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## OM protein - Protein search, using sw model

Run on: September 24, 2004, 07:28:32 ; Search time 203.368 Seconds

(without alignments)

116.704 Million cell updates/sec

Title: US-09-498-556C-59

Perfect score: 486

Sequence: 1 KATMOCGENEKYDSGSKBC.....VSAEDCELDNMDFIYPGTRN 84

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 28254705 residues

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- A\_Geneseq\_29Jan04:\*
- 1: GeneseqP1998s:\*
- 2: GeneseqP1998s:\*
- 3: GeneseqP2000s:\*
- 4: GeneseqP2001s:\*
- 5: GeneseqP2002s:\*
- 6: GeneseqP2003s:\*
- 7: GeneseqP2003s:\*
- 8: GeneseqP2003s:\*

## RESULT 1

AY30432

ID AY30432 standard; protein; 84 AA.

XX

AY30432;

AC

XX

DT 15-NOV-1999 (first entry)

XX

DE Mature nematode extracted anticoagulant protein AcaNAPc2.

XX

NM Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; factor VIIa/TF.

KW XX

OS OS

Ancylostoma caninum.

XX

PN PN

USS955294 A.

XX

PD 21-SEP-1999.

XX

PP 19-APR-1996;

XX

96US-00634641.

PP XX

PR 18-OCT-1994;

XX

94US-00326110.

PR XX

95US-004195;

XX

95US-0045380.

PR XX

05-JUN-1995;

XX

95US-0046397.

PR XX

05-JUN-1995;

XX

95US-0046399.

PR XX

17-OCT-1995;

XX

95WO-US032331.

PR XX

(CORV-) CORVAS INT INC.

PA XX

Lawrence MJ, Stanssens PEH, Jaspers LS, Gansmans YGU, Moyle M;

PI PI

Bergum PW, Messens JHL, Laroche YR, Vlaesuk GP;

XX XX

WPI 1999-539569/45.

XX XX

Screening an isolated protein for Nematode-extracted Anticoagulant

PT PT

Protein domains.

XX XX

Disclosure; Col 142-144 197pp; English.

PS PS

The present sequence represents a nematode extracted anticoagulant

CC CC

protein (NAP). The protein contains at least one NAP domain which

CC CC

protease inhibitor. The protein has activity for factor VIIa/TF.

CC CC

The specific specification

CC CC

describes a method for screening an isolated protein at least one domain

CC CC

for factor VIIa/TF selective inhibitory activity. The method comprises

CC CC

determining the time to clotting effected by a concentration of the

CC CC

isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo

CC CC

assay and an ex vivo

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	84	2 AY30432	Aay30432 Nature ne
2	486	100.0	84	3 AAB15317	Aab15317 A. caninu
3	486	100.0	91	2 AAR91701	Aar91701 AcaNAPc2.
4	486	100.0	91	2 AAY30393	Aay30393 Nematode
5	486	100.0	91	2 AAY30454	Aay30454 Nematode
6	486	100.0	91	3 AAB15346	Aab15346 A. caninu
7	212	43.6	82	2 AAY30422	Aay30422 Nature ne
8	212	43.6	82	2 AAY30399	Aay30399 Nematode
9	212	43.6	82	3 AAB15293	Aab15293 A. ceylan
10	212	43.6	82	3 AAB15307	Aab15307 A. ceylan
11	212	43.6	171	2 AAY30435	Aay30435 Nature ne
12	212	43.6	190	2 AAR91710	Aar91710 AceNAPc2.
13	212	43.6	190	2 AAY30384	Aay30384 Nematode
14	202	41.6	86	2 AAY30419	Aay30419 Nature ne
15	202	41.6	86	3 AAB15304	Aab15304 A. caninu
16	202	41.6	105	2 AAR91708	Aar91708 AcaNAPc4.
17	202	41.6	105	2 AAY30421	Aay30421 Nematode
18	201	41.4	89	2 AAY30428	Aay30428 Nature ne
19	201	41.4	108	2 AAY30398	Aay30398 Nematode
20	199	40.9	108	2 AAB15292	Aab15292 A. ceylan
21	199	40.9	86	2 AAY30418	Aay30418 Nature ne
22	199	40.9	86	3 AAB15303	Aab15303 A. caninu
23	199	40.9	105	2 AAY91707	Aay91707 AcaNAPc5.
24	199	40.9	105	2 AAY30406	Aay30406 Nematode
25	197.5	40.6	88	2 AAY30416	Aay30416 Nature ne

activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay; with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.

Sequence 84 AA;

CC	activated partial thromboplastin time (aPTT) assay; calculating
CC	prolongation of clotting effected by the isolated protein in each of the
CC	PT and aPTT assay. Pred. No. 4.2e-38;
CC	assay, where prolongation of clotting is calculated as fold elevation of
CC	clotting time relative to a baseline clotting value, where a doubling of
CC	clotting time is deemed a two-fold elevation; and calculating a PT to
CC	aPTT prolongation ratio, where a ratio at least one is indicative of
CC	factor VIIa/TF inhibitory activity. The method is useful for determining
CC	if a protein has factor VIIa/TF inhibitory activity

XX Sequence 84 AA;

Query Match Score 486; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.2e-38;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KATMOCGENEKYDSCGSKEDRKCKYDSEEEDEEPNVPCLVRVCHQDCVCEEGFYRNX 60
Db 1 KATMOCGENEKYDSCGSKEDRKCKYDSEEEDEEPNVPCLVRVCHQDCVCEEGFYRNX 60
Qy 61 DDKCVSAECDLNDMDFIYPGTRN 84
Db 61 DDKCVSAECDLNDMDFIYPGTRN 84

RESULT 2

AAB15317 standard protein; 84 AA.

XX	AAB15317
AC	AC
XX	06-AUG-2003 (revised)
DT	19-DEC-2000 (first entry)
XX	A. caninum nematode-extracted anticoagulant protein AcaNAPc2 (mature).
DE	KW Nematode-extracted anticoagulant protein; AcaNAPc2; blood clotting;
XX	KW canine hookworm; thrombosis; vaccine.
XX	Ancylostoma caninum.
OS	US2007447-A.
XX	PA WO9612021-A2.
XX	XX
PD	11-JUL-2000.
XX	XX
PF	12-FEB-1999; 99US-00249451.
XX	XX
PR	18-OCT-1994; 94US-00326110.
PR	05-JUN-1995; 95US-00461965.
PR	05-JUN-1995; 95US-00465380.
PR	05-JUN-1995; 95US-00486397.
PR	05-JUN-1995; 95US-00463399.
PR	17-OCT-1995; 95WO-US013231.
PR	18-OCT-1994; 94US-00326110.
PR	05-JUN-1995; 95US-00461965.
PR	05-JUN-1995; 95US-00465380.
PR	05-JUN-1995; 95US-00486397.
PR	05-JUN-1995; 95US-00486399.
XX	PA (CORY-) CORVAS INT INC.
PA	XX
XX	PI Vlasak GP, Stanssens PEH, Messens JHL, Lauwers MJ, Laroche YR;
DR	PI PI Jespers LS, Gansmans YGJ, Moyle M, Bergum PW;
N-PSDB; AAA73373.	XX DR WPI; 1996-222007/22.

XX	Proteins with anticoagulant and/or serine protease inhibitory activity -
XX	New cDNA molecule encoding a protein having factor Xa inhibitory activity
PT	for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains.
PT	Example A; Fig 16; 197pp; English.
PT	The present sequence is the Ancylostoma caninum nematode-extracted
CC	anticoagulant protein AcaNAPc2. Proteins of this kind have been shown to
CC	be effective preventing blood clotting without causing excessive
CC	bleeding. The protein can be used in blood collection tubes to aid the

isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes (the coding sequence can also be used for this) or as diagnostic tests. The protein can also be used as a vaccine against nematode parasites. (Updated on 06-AUG-2003 to correct OS field.)

SQ Sequence 84 AA;

Query Match Score 486; DB 3; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.2e-38;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KATMOCGENEKYDSCGSKEDRKCKYDSEEEDEEPNVPCLVRVCHQDCVCEEGFYRNX 60
Db 1 KATMOCGENEKYDSCGSKEDRKCKYDSEEEDEEPNVPCLVRVCHQDCVCEEGFYRNX 60
Qy 61 DDKCVSAECDLNDMDFIYPGTRN 84
Db 61 DDKCVSAECDLNDMDFIYPGTRN 84

RESULT 3

AAR91701

ID AAR91701 standard protein; 91 AA.	
XX	XX
AC	AC
XX	25-MAR-2003 (revised)
DT	17-NOV-1996 (first entry)
XX	XX
ACANAPC2.	XX
XX	AcANAP; HpONAP; NamNAP; AceNAP; AduNAP; anticoagulant;
KW	nematode-extracted anticoagulant protein; serine protease; nematode;
KW	thrombosis; parasitic worm.
XX	XX
OS Ancylostoma caninum.	OS
XX	XX
PN WO9612021-A2.	PN
XX	XX
PD 25-APR-1996.	PD
XX	XX
PF 17-OCT-1995;	PF
XX	XX
PR 94US-00326110.	PR
PR 95US-00461965.	PR
PR 95US-00465380.	PR
PR 95US-00486397.	PR
PR 95US-00463399.	PR
PR 95US-00486399.	PR
XX	PA (CORY-) CORVAS INT INC.
PA	XX
XX	PI Vlasak GP, Stanssens PEH, Messens JHL, Lauwers MJ, Laroche YR;
DR	PI PI Jespers LS, Gansmans YGJ, Moyle M, Bergum PW;
N-PSDB; AAA73373.	XX DR WPI; 1996-222007/22.

XX	Proteins with anticoagulant and/or serine protease inhibitory activity,
CC	isolated from nematodes, are useful to inhibit blood coagulation. The
CC	proteins can be added to blood collection tubes defining the collection
CC	of mammalian plasma. They are also useful to prevent or inhibit
CC	thrombosis, and may be given alone or in combination with other
CC	therapeutic or in vivo diagnostic agents. The proteins can serve as

immunogens to raise antibodies for use in the diagnosis and identification of NAP concn. levels in biological fluids, e.g. to detect mammalian infection with a parasitic worm. They can also be used as immunogens in prophylactic and therapeutic vaccines against parasitic worm infection. The proteins may double the clotting time of human plasma when present at 10-50 nMol, and double the clotting time of human plasma in activated partial thrombin time assays when present at 10-100 nMol. The anticoagulant proteins are pref. derived from Acanthostoma caninum, A. ceylanicum, A. duodenale, Necator americanus or Heligmosomoides polygyrus. The proteins pref. have 2 NAP domains and specifically inhibit the catalytic activity of the factor VIIa/TF complex in the presence of factor Xa or a catalytically inactive factor Xa deriv., do not specifically inhibit the activation of factor VIIa in the absence of TF and do not specifically inhibit prothrombinase. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 91 AA;

Query Match 100.0%; Score 486; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 4.6e-38;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX

Qy 1 KATMQCGENEKYDSSGSKEDKKCKYDVEEEDEEPNVPCLVRCHQDDCVCEEGFYRNK 60  
Db 8 KATMQCGENEKYDSSGSKEDKKCKYDVEEEDEEPNVPCLVRCHQDDCVCEEGFYRNK 67

Qy 61 DDKCVSAEDCELMDMFYFGTRN 84  
Db 68 DDKCVSAEDCELMDMFYFGTRN 91

RESULT 4

AY30393 standard; protein: 91 AA.  
XX  
AC AY30393;  
XX  
DT 15-NOV-1999 (first entry)  
DE Nematode extracted anticoagulant protein AcanAPC2.  
KW Nematode extracted anticoagulant protein; NAP; anticoagulant;  
KW serine protease inhibitor; NAP domain; factor VIIa/TF.  
XX  
Acanthostoma caninum.  
OS XX  
PN US555294-A.  
XX  
PD 21-SEP-1999.  
XX  
PF 19-APR-1996; 96US-00634641.  
XX  
PR 18-OCT-1994; 94US-00326110.  
PR 05-JUN-1995; 95US-00461665.  
PR 05-JUN-1995; 95US-00465380.  
PR 05-JUN-1995; 95US-00486397.  
PR 05-JUN-1995; 95US-00486399.  
PR 17-OCT-1995; 95WO-US013231.

(CORV-) CORVAS INT INC.

Lauwers MJ, Stanssens PEH, Jaspers LS, Gansmans YGJ, Moyle M;  
Bergum PW, Messens JHL, Laroche YR, Vlasuk GP;  
WPI: 1999-539569/45.  
XX  
Screening an isolated protein for Nematode-extracted Anticoagulant Protein domains.  
XX  
Example 13: Fig 9; 197PP; English.  
XX  
The present sequence represents a nematode extracted anticoagulant

protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating the prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity

Sequence 91 AA;

Query Match 100.0%; Score 486; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 4.6e-38;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX

Qy 1 KATMQCGENEKYDSSGSKEDKKCKYDGYEEEDDEEPNVPCLVRCHQDDCVCEEGFYRNK 60  
Db 8 KATMQCGENEKYDSSGSKEDKKCKYDGYEEEDDEEPNVPCLVRCHQDDCVCEEGFYRNK 67

Qy 61 DDKCVSAEDCELMDMFYFGTRN 84  
Db 68 DDKCVSAEDCELMDMFYFGTRN 91

RESULT 5

AY30394 standard; protein: 91 AA.  
XX  
AC AY30394;  
XX  
DT 15-NOV-1999 (first entry)  
DE Nematode extracted anticoagulant protein AcanAPC2.  
XX  
Nematode extracted anticoagulant protein; NAP; anticoagulant;  
KW serine protease inhibitor; NAP domain; factor VIIa/TF.  
XX  
Acanthostoma caninum.  
OS XX  
PN US555294-A.  
XX  
PD 21-SEP-1999.  
XX  
PF 19-APR-1996; 96US-00634641.  
XX  
PR 18-OCT-1994; 94US-00326110.  
PR 05-JUN-1995; 95US-00461665.  
PR 05-JUN-1995; 95US-00465380.  
PR 05-JUN-1995; 95US-00486397.  
PR 05-JUN-1995; 95US-00486399.  
PR 17-OCT-1995; 95WO-US013231.  
XX  
(CORV-) CORVAS INT INC.

XX  
Lauwers MJ, Stanssens PEH, Jaspers LS, Gansmans YGJ, Moyle M;  
Bergum PW, Messens JHL, Laroche YR, Vlasuk GP;  
WPI: 1999-539569/45.  
XX  
Screening an isolated protein for Nematode-extracted Anticoagulant Protein domains.  
XX  
Disclosure; Col 175-176; 197PP; English.  
XX  
The present sequence represents a nematode extracted anticoagulant

CC protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating the prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity

XX  
Sequence 91 AA;

Query Match 100.0%; Score 486; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 4.6e-38;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX

Qy 1 KATMQCGENEKYDSSGSKEDKKCKYDGYEEEDDEEPNVPCLVRCHQDDCVCEEGFYRNK 60  
Db 8 KATMQCGENEKYDSSGSKEDKKCKYDGYEEEDDEEPNVPCLVRCHQDDCVCEEGFYRNK 67

Qy 61 DDKCVSAEDCELMDMFYFGTRN 84  
Db 68 DDKCVSAEDCELMDMFYFGTRN 91

protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specification for factor VIIa/TF selective inhibitor activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating the prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.

XX Sequence 91 AA;

Query Match	100.0%	Score 486;	DB 2;	Length 91;
Best Local Similarity	100.0%	Pred. No. 4	6e-38;	
Matches	84;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

Qy 1 KATHQCGENEKYDGSKECDKCKYDVEEDEPNVCLVRVHQDCYCEEGFYRNIK 60  
Db 8 KATHQCGENEKYDGSKECDKCKYDVEEDEPNVCLVRVHQDCYCEEGFYRNIK 67

Qy 61 DDKCVSAEDCELNDMDFIYPGTRN 84  
Db 68 DDKCVSAEDCELNDMDFIYPGTRN 91

## RESULT 6

AAB15346 standard; protein; 91 AA.  
ID AAB15346;

XX AC 06-AUG-2003 (revised)  
DT 19-DEC-2000 (first entry)

XX DE A. caninum nematode-extracted anticoagulant protein AcanAPc2.

XX KW Nematode-extracted anticoagulant protein; NAP; anticoagulant; canine hookworm; thrombosis; vaccine.  
XX OS Ancylostoma caninum.  
XX PN US6087447-A.  
XX PD 11-JUL-2000.  
XX PF 12-FEB-1999; 99US-00249451.  
XX PR 18-OCT-1994; 94US-00326110.  
PR 05-JUN-1995; 95US-00461965.  
PR 05-JUN-1995; 95US-00461965.  
PR 05-JUN-1995; 95US-00465380.  
PR 05-JUN-1995; 95US-00486397.  
PR 05-JUN-1995; 95US-00486399.  
PR 17-OCT-1995; 95WO-US013231.  
PR 17-APR-1997; 97US-00809455.

XX PA (CORV-) CORVAS INT INC.

XX PA Lauwerays MJ, Stanssens PEH, Jaspers LS, Gansmans YGJ, Moyle M;  
PI Bergum PW, Messens JH, Laroche YR, Viasuk GP;

XX DR WPI: 2000-531359/48.  
DR N-PSDB; AAA7373.

XX PS New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains.

XX PT The present sequence represents a nematode-extracted anticoagulant

XX Disclosure; Fig 11; 197pp; English.  
PS XX The present sequence is the Acanlostoma caninum nematode-extracted CC anti-coagulant protein AcanAPc2. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The protein can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes (the coding sequence can also be used for this) or as diagnostic tests. The protein can also be used as a vaccine against nematode parasites. (Updated on 06-AUG-2003 to correct OS field.)

XX SQ Sequence 91 AA;

Query Match	100.0%	Score 486;	DB 3;	Length 91;
Best Local Similarity	100.0%	Pred. No. 4	6e-38;	
Matches	84;	Conservative	0;	Mismatches 0;
Indels	0;	Gaps	0;	

Qy 1 KATHQCGENEKYDGSKECDKCKYDVEEDEPNVCLVRVHQDCYCEEGFYRNIK 60  
Db 8 KATHQCGENEKYDGSKECDKCKYDVEEDEPNVCLVRVHQDCYCEEGFYRNIK 67

Qy 61 DDKCVSAEDCELNDMDFIYPGTRN 84  
Db 68 DDKCVSAEDCELNDMDFIYPGTRN 91

## RESULT 7

AAY30422 standard; protein; 82 AA.  
ID AAY30422;  
XX AC AAY30422;

XX DT 15-NOV-1999 (first entry)

XX DE Mature nematode extracted anticoagulant protein AceNAP4d2.

XX KW Nematode extracted anticoagulant inhibitor; NAP domain; factor VIIa/TF; serine protease inhibitor; NAP domain; factor VIIa/TF.  
XX OS Ancylostoma ceylanicum.  
XX PN US5955294-A.

XX PD 21-SEP-1999.

XX PP 19-APR-1996;

XX PR 96US-00634461.

XX PR 18-OCT-1994; 94US-00326110.  
PR 05-JUN-1995; 95US-00461965.  
PR 05-JUN-1995; 95US-00465380.

XX PR 05-JUN-1995; 95US-00486397.

XX PR 05-JUN-1995; 95US-00486399.

XX PR 17-OCT-1995; 95WO-US013231.

XX PA (CORV-) CORVAS INT INC.

XX PI Lauwerays MJ, Stanssens PEH, Jaspers LS, Gansmans YGJ, Moyle M;  
PI Bergum PW, Messens JH, Laroche YR, Viasuk GP;

XX DR WPI: 1999-530569/45.

XX PS Screening an isolated protein for Nematode-extracted Anticoagulant Protein Domains.

XX PS Disclosure; Col 135-136; 197pp; English.

XX CC The present sequence represents a nematode-extracted anticoagulant

protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specificity describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.

Sequence 82 AA;

Query Match	43.6%	Score 212;	DB 2;	Length 82;
Best Local Similarity	50.0%	Pred. No. 1	6e-12;	
Matches	38;	Conservative	11;	Mismatches 19;
AC		Indels	8;	Gaps 3;

Qy 6 CGENEKYDSCGS-KECDKCKYDGVFEDDEEEVNPCLVRVCHQD--CVCEEGFYRNKDD 62  
Db 4 CGSNERYSDGNDKQCERKCNEDDVYERGDE----ACRSHVCERPGACVCFYRNKKG 58

Qy 63 KCVSAEDCDELNNMDFI 78  
Db 59 SCVSESDCCEYDNMDFI 74

RESULT 8

AAY30399 AAY30399 standard; protein, 82 AA.  
XX

AAY30399;

XX DT 15-NOV-1999 (first entry)

DE Nematode extracted anticoagulant protein AcenAP4d2.

XX KW Nematode extracted anticoagulant protein; NAP; anticoagulant;  
KW serine protease inhibitor; NAP domain; factor VIIa/TF.  
OS XX Ancylostoma ceylanicum.  
PN XX US59555294-A.

XX PD 21-SEP-1999.

XX PF 19-APR-1996;

XX 96US-00634641.

PR 18-OCT-1994; 94US-00326110.  
PR 05-JUN-1995; 95US-0041955.  
PR 05-JUN-1995; 95US-00465380.  
PR 05-JUN-1995; 95US-00486397.  
PR 05-JUN-1995; 95US-00486399.  
PR 17-OCT-1995; 95WO-US013221.

XX (CORV-) CORVAS INT INC.

XX Lauwereys MJ, Stanssens PBH, Jespers LS, Gansmans YGJ, Moyle M;  
PI Bergum PW, Messens JHL, Laroche YR, Viasuk GP;  
XX WPI; 1999-539569/45.

XX PR Screening an isolated protein for Nematode-extracted Anticoagulant Protein domains.  
XX Disclosure; Col 111-112; 197pp; English.

CC The present sequence represents a nematode extracted anticoagulant

protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specificity describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.

Sequence 82 AA;

Query Match	43.6%	Score 212;	DB 2;	Length 82;
Best Local Similarity	50.0%	Pred. No. 1	6e-12;	
Matches	38;	Conservative	11;	Mismatches 19;
AC		Indels	8;	Gaps 3;

Qy 6 CGENEKYDSCGS-KECDKCKYDGVFEDDEEEVNPCLVRVCHQD--CVCEEGFYRNKDD 62  
Db 4 CGSNERYSDGNDKQCERKCNEDDVYERGDE----ACRSHVCERPGACVCFYRNKKG 58

Qy 63 KCVSAEDCDELNNMDFI 78  
Db 59 SCVSESDCCEYDNMDFI 74

RESULT 9

AAB15293 AAB15293 standard; protein, 82 AA.  
XX AC AAB15293;

XX DT 06-AUG-2003 (revised)  
DT 19-DEC-2000 (first entry)

DE A. ceylanicum nematode-extracted anticoagulant protein AcenAP4d2 #1.  
XX KW Nematode-extracted anticoagulant protein; AcenAP4d2; blood clotting;  
KW canine hookworm; thrombosis; vaccine.  
OS XX Ancylostoma ceylanicum.  
XX US6087487-A.

XX PD 11-JUL-2000.

XX PF 12-FEB-1999;

XX 99US-00249451.  
PR 18-OCT-1994; 94US-00326110.  
PR 05-JUN-1995; 95US-0041955.  
PR 05-JUN-1995; 95US-00465380.  
PR 05-JUN-1995; 95US-00486397.  
PR 05-JUN-1995; 95US-00486399.  
PR 17-OCT-1995; 95WO-US013221.  
PR 17-OCT-1995; 95WO-US013231.  
PR 17-APR-1997; 97US-0089455.

XX (CORV-) CORVAS INT INC.

XX PA Lauwereys MJ, Stanssens PBH, Jespers LS, Gansmans YGJ, Moyle M;  
PI Bergum PW, Messens JHL, Laroche YR, Viasuk GP;  
XX DR WPI; 2000-531359/48.

XX PT New cDNA molecule encoding a protein having factor Xa inhibitory activity  
PT for preventing and treating blood clotting disorders, comprises nematode-  
PT extracted anticoagulant protein domains.  
XX

Disclosure; Fig 11; 197pp; English.

The present sequence is the *Ancylostoma ceylanicum* nematode-extracted anticoagulant protein AcenAP4d2. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The protein can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes or as diagnostic tests. The protein can also be used as a vaccine against nematode parasites. (Updated on 06-AUG-2003 to correct OS field.)

XX Sequence 82 AA;  
 SQ      Query Match 43.6%; Score 212; DB 3; Length 82;  
 ID      Best Local Similarity 50.0%; Pfd. No. 1.6e-12;  
 AC      Matches 38; Conservative 11; Mismatches 19; Indels 8; Gaps 3;  
 DT      QY 6 CGENEKYDSCGS-KECDKCKYDGVEEBDEDPNVPCLVRYCHQD--CVCBEGFYRKND 62  
 DE 4 CGSNERYSPCGNDKQCEBKCNEDDYEGDE----ACRSHVCPGACVCEGDFYRKKG 58  
 KW QY 63 KCVSAEDCFLDNDMFI 78  
 OS Db 59 SCVESDDCEYDNDFI 74

RESULT 10

AAB15307 standard; protein; 82 AA.

XX AAB15307;  
 XX DT 06-AUG-2003 (revised)  
 XX 19-DEC-2000 (first entry)  
 XX A. ceylanicum nematode-extracted anticoagulant protein AcenAP4d2 #2.  
 XX Nematode-extracted anticoagulant protein; AcenAP4d2; blood clotting;  
 XX canine hookworm; thrombosis; vaccine.  
 XX OS *Ancylostoma ceylanicum*.  
 XX PN US6087487-A.  
 XX PD 11-JUL-2000.  
 XX PF 12-FEB-1999; 99US-00249451.  
 XX PR 18-OCT-1994; 94US-00326110.  
 PR 05-JUN-1995; 95US-00461965.  
 PR 05-JUN-1995; 95US-00465350.  
 PR 05-JUN-1995; 95US-00486339.  
 PR 05-JUN-1995; 95US-00486339.  
 PR 17-OCT-1995; 95WO-US013231.  
 PR 17-APR-1997; 97US-00809455.

XX (CORV-) CORVAS INT INC.  
 XX PI Lauwereys MJ, Stanssens PEH, Jespers LS, Gansmans YGJ, Moyle M;  
 PA Bergum PW, Messens JHL, Laroche YR, Vlasuk GP;  
 XX WPI; 1999-539569/45.  
 PI Lauwereys MJ, Stanssens PEH, Jespers LS, Gansmans YGJ, Moyle M;  
 PI Bergum PW, Messens JHL, Laroche YR, Vlasuk GP;  
 XX WPI; 2000-531359/48.  
 XX PT New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains.  
 XX Disclosure; Fig 16; 197pp; English.

XX The present sequence is the *Ancylostoma ceylanicum* nematode-extracted anticoagulant protein AcenAP4d2. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The protein can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes or as diagnostic tests. The protein can also be used as a vaccine against nematode parasites. (Updated on 06-AUG-2003 to correct OS field.)

XX Sequence 82 AA;  
 SQ      Query Match 43.6%; Score 212; DB 3; Length 82;  
 ID      Best Local Similarity 50.0%; Pfd. No. 1.6e-12;  
 AC      Matches 38; Conservative 11; Mismatches 19; Indels 8; Gaps 3;  
 DT      QY 6 CGENEKYDSCGS-KECDKCKYDGVEEBDEDPNVPCLVRYCHQD--CVCBEGFYRKND 62  
 DE 4 CGSNERYSPCGNDKQCEBKCNEDDYEGDE----ACRSHVCPGACVCEGDFYRKKG 58  
 KW QY 63 KCVSAEDCFLDNDMFI 78  
 OS Db 59 SCVESDDCEYDNDFI 74

RESULT 11

AYA30435 standard; protein; 171 AA.

XX AAY30435;  
 XX AC AAY30435;  
 XX DT 15-NOV-1999 (first entry)  
 XX DE Mature nematode extracted anticoagulant protein AcenAP4.  
 XX KW Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; Factor VIIa/TF.  
 XX CS *Ancylostoma ceylanicum*.  
 XX PN US5955294-A.  
 XX PD 21-SEP-1999.  
 XX PF 19-APR-1996;  
 XX PR 18-OCT-1994; 94US-00326110.  
 PR 05-JUN-1995; 95US-00461965.  
 PR 05-JUN-1995; 95US-00465380.  
 PR 05-JUN-1995; 95US-00483397.  
 PR 05-JUN-1995; 95US-00486339.  
 PR 17-OCT-1995; 95WO-US013231.  
 XX PA (CORV-) CORVAS INT INC.  
 XX PI Lauwereys MJ, Stanssens PEH, Jespers LS, Gansmans YGJ, Moyle M;  
 PA Bergum PW, Messens JHL, Laroche YR, Vlasuk GP;  
 XX WPI; 1999-539569/45.  
 PI Lauwereys MJ, Stanssens PEH, Jespers LS, Gansmans YGJ, Moyle M;  
 PI Bergum PW, Messens JHL, Laroche YR, Vlasuk GP;  
 XX WPI; 2000-531359/48.  
 XX PT Screening an isolated protein for Nematode-extracted Anticoagulant Protein domains.  
 XX Disclosure; Fig 17; 197pp; English.

XX The present sequence represents a nematode extracted anticoagulant and/or serine protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which

has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating the prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.

SQ Sequence 171 AA;

Query Match Score 212; DB 2; Length 171;  
Best Local Similarity 50.0%; Pred. No. 3.5e-12; Gaps 3;

Matches 38; Conservative 11; Mismatches 19; Indels 8;

CC 6 CGENEKYVSCGS-KECDKCKYDGVEEEDDEPVPCLVRYCHQ--CVCEEGFYRNKKD 62

Db 93 CGENERYSDGNDKQCERKCNEDDYERKDE----ACRSHVCPGACYCVDGFTRNKG 147

QY 63 KCVSAEDCFLDNMDFI 78

Db 148 SCYESDDCEYDNMDFI 163

SQ Sequence 190 AA;

Query Match Score 212; DB 2; Length 190;  
Best Local Similarity 50.0%; Pred. No. 3.9e-12; Gaps 3;

Matches 38; Conservative 11; Mismatches 19; Indels 8;

CC 6 CGENBKRYDSCGS-KECDKCKYDGVEEEDDEPVPCLVRYCHQ--CVCEEGFYRNKKD 62

Db 112 CGSNRYSQDGNDKQCERKCNEDDYERKDE----ACRSHVCPGACYCVDGFTRNKG 166

QY 63 KCVSAEDCFLDNMDFI 78

Db 167 SCVESDDCEYDNMDFI 182

SQ Sequence 190 AA;

RESULT 13 AAY30384 standard; protein; 190 AA.

ID AAY30384 standard; protein; 190 AA.

XX AC AAY30384;

XX DT 15-NOV-1999 (First entry)

XX DE Nematode extracted anticoagulant protein AcenAP4.

XX KW Nematoide extracted anticoagulant protein; NAP domain; factor VIIa/TF.

XX OS Ancylostoma ceylanicum.

XX PN US5955294-A.

XX PR 21-SEP-1999.

XX PR 19-APR-1996;

XX PR 05-JUN-1995;



PA (CORVAS INT INC.  
 XX Lauwereys MJ, Stanssens PBH, Jespers LS, Gansmans YGJ, Moyle M;  
 PI Bergum PW, Messens JHL, Laroche YR, Vlasuk GP;  
 XX DR WPI: 2000-531359-48.  
 DR N-PSDB; AAA73379.  
 XX PT New cDNA molecule encoding a protein having factor Xa inhibitory activity  
 PT for preventing and treating blood clotting disorders, comprises nematode-  
 PT extracted anticoagulant protein domains.  
 XX Disclosure; Fig 16; 197pp; English.  
 XX The present sequence is the Ancylostoma caninum nematode-extracted  
 CC anticoagulant protein AcalAP44. Proteins of this kind have been shown to  
 CC be effective at preventing blood clotting without causing excessive  
 CC bleeding. The protein can be used in blood collection tubes to aid the  
 CC isolation of plasma from the blood, to prevent thrombosis which may be  
 CC linked to the rupture of an atherosclerotic plaque, acute myocardial  
 CC infarction, angina, thrombolytic therapy, percutaneous transluminal  
 CC coronary angioplasty, disseminated intravascular coagulopathy, infection,  
 CC cancer and septic shock, and to produce antibodies. In the latter  
 CC instance, the antibodies can be raised in order to detect infection by  
 CC nematodes (the coding sequence can also be used for this) or as  
 CC diagnostic tests. The protein can also be used as a vaccine against  
 CC nematode parasites. (Updated on 06-AUG-2003 to correct OS Field.)  
 XX Sequence 86 AA;

Query Match Score 202; DB 3; Length 86;  
 Best Local Similarity 41.6%; Pred. No. 1.5e-11;  
 Matches 37; Conservative 15; Mismatches 22; Indels 4; Gaps 2;  
 Qy 5 OCGENEKYDSCGSKECDKCKYDGVERBDD--EEPNVPCLYRVHQ--DCVCEEGFYRK 60  
 Db 5 KCPGERIDCANKPCEPKKIEETSEBBDDVEETDVRCLVRCERPLKCIKRDGYRK 64  
 Qy 61 DDKCVSAEDCELDNMDFT 78  
 Db 65 KGBCVTDIVCQEDFMEFT 82

Search completed: September 24, 2004, 07:34:15  
 Job time : 204.368 secs

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Gencore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: September 24, 2004, 07:30:36 ; Search time 52.1684 Seconds

(without alignments)  
83.127 Million cell updates/sec

Title: US-09-498-556C-39

Perfect score: 486

Sequence: 1 KATMQCGEREKYDSGSKBC.....VSADCELDNMDPIYPGTRN 84

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 0%  
Listing first 45 summaries

Database : Issued Parents AA:\*

1: /sgn2\_6/ptodata/2/iaa1SA\_COMBO.pep:\*
 2: /sgn2\_6/ptodata/2/iaa1SB\_COMBO.pep:\*
 3: /sgn2\_6/ptodata/2/iaa16A\_COMBO.pep:\*
 4: /sgn2\_6/ptodata/2/iaa16B\_COMBO.pep:\*
 5: /sgn2\_6/ptodata/2/iaa1FC1US\_COMBO.pep:\*
 6: /sgn2\_6/ptodata/2/iaa1bachfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	486	100.0	84	2	US-08-465-380-59	Sequence 59, App1
2	486	100.0	84	2	US-08-486-397-59	Sequence 59, App1
3	486	100.0	84	2	US-08-496-399-59	Sequence 59, App1
4	486	100.0	84	2	US-08-451-965-59	Sequence 59, App1
5	486	100.0	84	2	US-08-634-641-59	Sequence 59, App1
6	486	100.0	84	3	US-09-24.9-471-59	Sequence 59, App1
7	486	100.0	84	3	US-09-24.9-472-59	Sequence 59, App1
8	486	100.0	84	3	US-09-24.9-451-59	Sequence 59, App1
9	486	100.0	84	3	US-08-809-455-59	Sequence 59, App1
10	486	100.0	84	3	US-09-24.9-461-59	Sequence 59, App1
11	486	100.0	84	3	US-09-24.9-448-59	Sequence 59, App1
12	486	100.0	84	4	US-09-24.9-473-59	Sequence 59, App1
13	486	100.0	91	2	US-08-495-380-128	Sequence 128, App1
14	486	100.0	91	2	US-08-490-478-50	Sequence 50, App1
15	486	100.0	91	2	US-08-486-397-128	Sequence 128, App1
16	486	100.0	91	2	US-08-486-399-128	Sequence 128, App1
17	486	100.0	91	2	US-08-463-965-128	Sequence 128, App1
18	486	100.0	91	2	US-08-328-11A-50	Sequence 50, App1
19	486	100.0	91	2	US-08-634-641-128	Sequence 128, App1
20	486	100.0	91	3	US-09-24.9-471-128	Sequence 128, App1
21	486	100.0	91	3	US-09-24.9-472-128	Sequence 128, App1
22	486	100.0	91	3	US-09-24.9-451-128	Sequence 128, App1
23	486	100.0	91	3	US-08-809-455-128	Sequence 128, App1
24	486	100.0	91	3	US-09-24.9-461-128	Sequence 128, App1
25	486	100.0	91	4	US-09-24.9-448-128	Sequence 128, App1
26	486	100.0	91	4	US-09-24.9-471-128	Sequence 128, App1
27	43.6	92	2	US-08-465-380-25	Sequence 25, App1	

## ALIGNMENTS

RESULT: 1  
 US-08-465-380-59  
 / Sequence 59, Application US/08465380  
 / Patent No. 5863384  
 / GENERAL INFORMATION:  
 / APPLICANT: George P. Vlasiuk, Patric H. Stanssens,  
 / Joris H.L. Mensens, Marc J. Lauwers,  
 / Yves R. Larche, Laurent S. Jespers,  
 / G. J. Gansmans, Matthew Moyle,  
 / Peter W. Bergum  
 / TITLE OF INVENTION: NEURONDE-EXTRACTED ANTICOGULANT  
 / NUMBER OF SEQUENCES: 356  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESS: Lyon & Lyon  
 / STREET: 633 West Fifth Street  
 / SUITE: Suite 4700  
 / CITY: Los Angeles  
 / STATE: California  
 / COUNTRY: U.S.A.  
 / ZIP: 90071  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 / MEDIUM TYPE: storage  
 / COMPUTER: IBM Compatible  
 / OPERATING SYSTEM: IBM P.C., DOS 5.0  
 / SOFTWARE: Word Perfect 5.1  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/08/465,380  
 / FILING DATE: June 5, 1995  
 / CLASSIFICATION: 530  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: 08/326,110  
 / FILING DATE: October 18, 1994  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: BIGGS, SUZANNE L.  
 / REGISTRATION NUMBER: 30,158  
 / REFERENCE/DOCKET NUMBER: 213/268  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: (213) 489-1600  
 / TELEFAX: (213) 955-0440  
 / TELEX: 67-3510  
 / INFORMATION FOR SEQ ID NO: 59:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 84 amino acids  
 / TYPE: amino acid  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: peptide  
 / ORIGINAL SOURCE:  
 / ORGANISM: Ancyclostoma caninum

US-08-465-380-59

Query Match 100.0%; Score 486; DB 2; Length 84;  
Best Local Similarity 100.0%; Pred. No. 4.7e-43;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 KATMOCGNEKYDSCSKECDKKCKYDGVEEDEEPNVPCLVYVCHQDCVCEGFYRNK 60  
Db 1 KATMOCGNEKYDSCSKECDKKCKYDGVEEDEEPNVPCLVYVCHQDCVCEGFYRNK 60

Qy 61 DDKCVSAEDCELDNDPIYPTRN 84  
Db 61 DDKCVSAEDCELDNDPIYPTRN 84

**RESULT 2**

US-08-486-397-59

Sequence 59, Application US/08486397

Patent No. 5866542

GENERAL INFORMATION:

APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
Joris H.L. Mensens, Marc J. Lawerens,  
Yves R. Laroche, Laurent S. Jaspers,  
APPLICANT: Yannick G.J. Ganssmuller, Matthew Moye,  
APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATOPE - EXTRACTED ANTICORAGULANT

NUMBER OF SEQUENCES: 357

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:

  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
  MEDIUM TYPE: storage  
  COMPUTER: IBM Compatible  
  OPERATING SYSTEM: IBM P.C., DOS 5.0  
  SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486, 397  
FILING DATE: June 5, 1995  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/326, 110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.

REGISTRATION DOCKET NUMBER: 30,158

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 59:

SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid  
TOPOLogy: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE: Anzylostoma caninum

US-08-486-397-59

Query Match 100.0%; Score 486; DB 2; Length 84;  
Best Local Similarity 100.0%; Pred. No. 4.7e-43;  
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy 1 KATMOCGNEKYDSCSKECDKKCKYDGVEEDEEPNVPCLVYVCHQDCVCEGFYRNK 60

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Db      1 KATMOCGENEKYDGGSKEDCDKCKYDGVVEEDDEEPNVPCLVRCHQDCVCEGFRNK 60
Qy      61 DDKCVSAEDCDLMDFIYPGTRN 84
Db      61 DDKCVSAEDCDLMDFIYPGTRN 84

RESULT 3
US-08-486-399-59
; Sequence 59, Application US/08486399
; Patent No. 5866543

; GENERAL INFORMATION:
;   APPLICANT: George P. Vlasuk, Patric H. Staessens,
;   APPLICANT: Joris H.L. Mensens, Marc J. Lauwersys,
;   APPLICANT: Yves R. Laroché, Laurent S. Jaspers,
;   APPLICANT: Yannick G.J. Ganssemans, Matthew Moyle,
;   APPLICANT: Peter W. Bergum
; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
; TITLE OF INVENTION: PROTIPIN
; NUMBER OF SEQUENCES: 356
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; ZIP: 90071
; COUNTRY: U.S.A.

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,399
; FILING DATE: June 5, 1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/326,110
; FILING DATE: October 18, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BIGGS, SUZANNE L.
; REGISTRATION NUMBER: 30,158
; REFERENCE/DOCKET NUMBER: 213/270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 84 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum
; US-08-486-399-59

Query Match          100.0%; Score 486; DB 2; Length 84;
Best Local Similarity 100.0%; Pred. No. 4.7e-51;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0
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D5      1 KATMOCGENEKYDGGSKEDCDKCKYDGVVEEDDEEPNVPCLVRCHQDCVCEGFRNK 60
Qy      61 DDKCVSAEDCDLMDFIYPGTRN 84
D5      61 DDKCVSAEDCDLMDFIYPGTRN 84

```

US-08-461-965-59

; Sequence 59, Application US/08461965

; Patent No. 5872098

GENERAL INFORMATION:

; APPLICANT: George P. Vlasek, Patric H. Stanssens,

; APPLICANT: Joris H.L. Mensens, Marc J. Lauwerys,

; APPLICANT: Yves R. Laroche, Laurent S. Jaspers,

; APPLICANT: Yannick G.J. Gansmans, Matthew Moyle,

; APPLICANT: Peter W. Bergum

; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

; NUMBER OF SEQUENCES: 356

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth street

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER: IBM Compatible

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: Word Perfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/461,965

; FILING DATE: June 5, 1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/326,110

; FILING DATE: October 18, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: BIGGS, SUZANNE L.

; REGISTRATION NUMBER: 30,158

; REFERENCE/DOCKET NUMBER: 210/243

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 59:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 84 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: Peptide

; ORIGINAL SOURCE:

; ORGANISM: Ancylostoma caninum

; US-08-461-965-59

Query Match 100.0%; Score 486; DB 2; Length 84;

Best Local Similarity 100.0%; Pred. No. 4,7e-43; Indels 0; Gaps 0;

Matches 84; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

US-08-634-641-59

Query Match 100.0%; Score 486; DB 2; Length 84;

Best Local Similarity 100.0%; Pred. No. 4,7e-43; Indels 0; Gaps 0;

Matches 84; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

Qy 1 KATMCGENKYDSSGSKEDDKCKYDGVEEEDDEPNPCLVRYCHQDCVYCERYNKRK 60

Db 1 KATMCGENKYDSSGSKEDDKCKYDGVEEEDDEPNPCLVRYCHQDCVYCERYNKRK 60

61 DDKCVSAEDCELDNMDFYPGTRN 84

61 DDKCVSAEDCELDNMDFYPGTRN 84

RESULT 5

US-08-634-641-59

; Sequence 59, Application US/08634641

; Patent No. 5955394

GENERAL INFORMATION:

; APPLICANT: Vlasek, George P. Vlasek

; APPLICANT: Stanssens, Patrick Eric Hugo

; APPLICANT: Mensens, Joris Hilda Lieven

; APPLICANT: Lauwerys, Marc Josef

RESULT 6

US-09-249-471-59

; Sequence 59, Application US/09249471

; Patent No. 6040441

APPLICANT: Laroche, Yves Rene  
 APPLICANT: Jaspers, Laurent Stephane  
 APPLICANT: Gansmans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew  
 APPLICANT: Bergum, Peter W.  
 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
 NUMBER OF SEQUENCES: 356  
 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
 NUMBER OF SEQUENCES: 356  
 ADDRESS: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/634,641  
 FILING DATE: April 19, 1996  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: FCT/US95/13231  
 FILING DATE: October 17, 1996  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 210/243  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum  
 US-08-461-965-59

Query Match 100.0%; Score 486; DB 2; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 4,7e-43; Indels 0; Gaps 0;  
 Matches 84; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

Qy 1 KATMCGENKYDSSGSKEDDKCKYDGVEEEDDEPNPCLVRYCHQDCVYCERYNKRK 60  
 Db 1 KATMCGENKYDSSGSKEDDKCKYDGVEEEDDEPNPCLVRYCHQDCVYCERYNKRK 60

Qy 1 KATMCGENKYDSSGSKEDDKCKYDGVEEEDDEPNPCLVRYCHQDCVYCERYNKRK 60  
 Db 1 KATMCGENKYDSSGSKEDDKCKYDGVEEEDDEPNPCLVRYCHQDCVYCERYNKRK 60

Qy 61 DDKCVSAEDCELDNMDFYPGTRN 84  
 Db 61 DDKCVSAEDCELDNMDFYPGTRN 84

RESULT 5  
 US-08-634-641-59  
 ; Sequence 59, Application US/08634641  
 ; Patent No. 5955394  
 GENERAL INFORMATION:  
 ; APPLICANT: Vlasek, George P. Vlasek  
 ; APPLICANT: Stanssens, Patrick Eric Hugo  
 ; APPLICANT: Mensens, Joris Hilda Lieven  
 ; APPLICANT: Lauwerys, Marc Josef

GENERAL INFORMATION  
 APPLICANT: Viasuk, George Phillip  
 APPLICANT: Stanssens, Patrick Eric Hugo  
 APPLICANT: Messens, Joris Hilda Lieven  
 APPLICANT: Lauwers, Marc Joseph  
 APPLICANT: Laroche, Yves Rene  
 APPLICANT: Jespers, Laurent Stephane  
 APPLICANT: Ganssemans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew  
 APPLICANT: Bergum, Peter W.  
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
 TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
 TITLE OF INVENTION: PROTEIN  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 613 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3 1/2" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C., DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/249,471  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/809,455  
 FILING DATE: April 17, 1997  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30-158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEFAX: 67-3510  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 ORIGINAL SOURCE: Ancylostoma caninum  
 US-09-249-471-59  
 Query Match Similarity 100.0%; Score 486; DB 3; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-13; Indels 0; Gaps 0;  
 Matches 84; Conservative 0; Mismatches 0;  
 Qy 1 KATMCGENEKYDSCGSKCDRKCKYDVEEDEEPCVLRVCHQDCVCEEGFYRNK 60  
 Db 1 KATMCGENEKYDSCGSKCDRKCKYDVEEDEEPCVLRVCHQDCVCEEGFYRNK 60

Db 61 DDKCVSAEDCELDNMDFIYPGTRN 84  
 RESULT 7  
 US-09-249-472-59  
 Sequence 59, Application US/09249472  
 ; Parent No. 6046318  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Viasuk, George Phillip  
 ; APPLICANT: Stanssens, Patrick Eric Hugo  
 ; APPLICANT: Messens, Joris Hilda Lieven  
 ; APPLICANT: Lauwers, Marc Joseph  
 ; APPLICANT: Laroche, Yves Rene  
 ; APPLICANT: Jespers, Laurent Stephane  
 ; APPLICANT: Ganssemans, Yannick Georges Jozef  
 ; APPLICANT: Moyle, Matthew  
 ; APPLICANT: Bergum, Peter W.  
 ; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
 ; TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
 ; TITLE OF INVENTION: PROTEIN  
 ; NUMBER OF SEQUENCES: 356  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 613 West Fifth Street  
 ; STREET: Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3 1/2" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C., DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/249,472  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/809,455  
 ; FILING DATE: April 17, 1997  
 ; APPLICATION NUMBER: PCT/US95/13231  
 ; FILING DATE: October 17, 1995  
 ; APPLICATION NUMBER: 08/486,399  
 ; FILING DATE: June 5, 1995  
 ; APPLICATION NUMBER: 08/486,397  
 ; FILING DATE: June 5, 1995  
 ; APPLICATION NUMBER: 08/465,380  
 ; FILING DATE: June 5, 1995  
 ; APPLICATION NUMBER: 08/461,965  
 ; FILING DATE: June 5, 1995  
 ; APPLICATION NUMBER: 08/326,110  
 ; FILING DATE: October 18, 1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BIGGS, SUZANNE L.  
 ; REGISTRATION NUMBER: 30-158  
 ; REFERENCE/DOCKET NUMBER: 216/270  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEFAX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 59:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 84 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Peptide  
 ; ORIGINAL SOURCE: Ancylostoma caninum  
 ; US-09-249-472-59  
 ; Query Match Similarity 100.0%; Score 486; DB 3; Length 84;  
 ; Best Local Similarity 100.0%; Pred. No. 4.7e-13; Indels 0; Gaps 0;  
 ; Matches 84; Conservative 0; Mismatches 0;  
 ; Qy 1 KATMCGENEKYDSCGSKCDRKCKYDVEEDEEPCVLRVCHQDCVCEEGFYRNK 60  
 ; Db 1 KATMCGENEKYDSCGSKCDRKCKYDVEEDEEPCVLRVCHQDCVCEEGFYRNK 60

Best Local Similarity 100.0%; Pred. No. 4.7e-43;  
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KATMQGENEKYDSCGKXECDKRCKYNGVEERDDEEPNVPCLVRCHQDCVCEEGFYRK 60  
 Db 1 KATMQGENEKYDSCGKXECDKRCKYNGVEERDDEEPNVPCLVRCHQDCVCEEGFYRK 60

RESULT 8  
 US-09-249-451-59  
 ; Sequence 59, Application US/09249451  
 ; Patent No. 608487  
 GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 APPLICANT: Stanssens, Patrick Eric Hugo  
 APPLICANT: Messens, Joris Hilda Lieven  
 APPLICANT: Lauwers, Marc Joseph  
 APPLICANT: Laroche, Yves Rene  
 APPLICANT: Jaspers, Laurent Stephane  
 APPLICANT: Gansmans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew  
 APPLICANT: Bergum, Peter W.  
 TITLE OF INVENTION: NEMATOIDE-EXTRACTED SERINE PROTEASE  
 TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
 NUMBER OF SEQUENCES: 356  
 CURRENT APPLICATION DATA:  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STREET: Suite 4700  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/249,451  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/809,455  
 FILING DATE: April 17, 1997  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/426,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids

TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE: Anacyclostoma caninum  
 US-09-249-451-59

Query Match 100.0%; Score 486; DB 3; Length 84;  
 Best Local Similarity 100.0%; Prc. No. 4.7e-43;  
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KATMQGENEKYDSCGKXECDKRCKYNGVEERDDEEPNVPCLVRCHQDCVCEEGFYRK 60  
 Db 1 KATMQGENEKYDSCGKXECDKRCKYNGVEERDDEEPNVPCLVRCHQDCVCEEGFYRK 60

RESULT 9  
 US-09-809-455-59  
 ; Sequence 59, Application US/08809455  
 ; Patent No. 6090916  
 GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 APPLICANT: Stanssens, Patrick Eric Hugo  
 APPLICANT: Messens, Joris Hilda Lieven  
 APPLICANT: Lauwers, Marc Joseph  
 APPLICANT: Laroche, Yves Rene  
 APPLICANT: Jaspers, Laurent Stephane  
 APPLICANT: Gansmans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew  
 APPLICANT: Bergum, Peter W.  
 TITLE OF INVENTION: NEMATOIDE-EXTRACTED SERINE PROTEASE  
 TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
 NUMBER OF SEQUENCES: 356  
 CURRENT APPLICATION DATA:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/809,455  
 FILING DATE: April 17, 1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/426,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids

TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum  
 US-08-809-455-59

Query Match Similarity 100.0%; Score 486; DB 3; Length 84;  
 Best Local Matches 84; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 KATMOCGENBKYTDSCGSKEDKCKYDGVVEBDDDEFNPCLVRVHQDCYCEEGFYRK 60  
 Db 1 KATMOCGENERTKYTDSCGSKEDKCKYDGVVEBDDDEFNPCLVRVHQDCYCEEGFYRK 60

Qy 61 DDKCVSAEDCELNMDFIYPGTRN 84  
 Db 61 DDKCVSAEDCELNMDFIYPGTRN 84

---

RESULT 10  
 US-09-249-461-59  
 Sequence 59, Application US/09249461  
 Patent No. 6096677

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 APPLICANT: Stanssens, Patrick Eric Hugo  
 APPLICANT: Messens, Joris Hilda Lieven  
 APPLICANT: Lauwers, Marc Joseph  
 APPLICANT: Jespers, Laurent Stephane  
 APPLICANT: Gansmans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew  
 APPLICANT: Bergum, Peter W.  
 APPLICANT: Lauwers, Yves Rene

TITLE OF INVENTION: NEMATO-E-EXTRACTED SERINE PROTEASE  
 INHIBITORS AND ANTICOAGULANT

TITLE OF INVENTION: PROTEIN  
 NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.

ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/249,461  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/809,455  
 FILING DATE: April 17, 1997  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965

---

FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/809,454  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGES, SUZANNE L.  
 REGISTRATION NUMBER: 30-158  
 REFERENCE/DOCKET NUMBER: 215/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEX: (213) 955-0440  
 TELEFAX: 67-3510

INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum

Query Match Similarity 100.0%; Score 486; DB 3; Length 84;  
 Best Local Matches 84; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 KATMOCGENBKYTDSCGSKEDKCKYDGVVEBDDDEFNPCLVRVHQDCYCEEGFYRK 60  
 Db 1 KATMOCGENBKYTDSCGSKEDKCKYDGVVEBDDDEFNPCLVRVHQDCYCEEGFYRK 60

Qy 61 DDKCVSAEDCELNMDFIYPGTRN 84  
 Db 61 DDKCVSAEDCELNMDFIYPGTRN 84

---

RESULT 11  
 US-09-249-448-59  
 Sequence 59, Application US/09249448  
 Patent No. 6121435

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 APPLICANT: Stanssens, Patrick Eric Hugo  
 APPLICANT: Messens, Joris Hilda Lieven  
 APPLICANT: Lauwers, Marc Joseph  
 APPLICANT: Laroché, Yves René  
 APPLICANT: Jespers, Laurent Stephane  
 APPLICANT: Gansmans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew  
 APPLICANT: Bergum, Peter W.  
 TITLE OF INVENTION: NEMATO-E-EXTRACTED SERINE PROTEASE  
 INHIBITORS AND ANTICOAGULANT  
 NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/249,448

FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/809,455  
 FILING DATE: April 17, 1997  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965

FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,961  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REFERENCE/DOCKET NUMBER: 30-158  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Anycyclostoma caninum  
 US-09-249-48-59

Query Match Score 486; DB 3; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 4.7e-43;  
 Matches 84; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 KATMQGENEKYDSCGSKEDCKCKYDGVEEDEPNVPLVRCHQDCVCEGFYRK 60  
 Db 1 KATMQGENEKYDSCGSKEDCKCKYDGVEEDEPNVPLVRCHQDCVCEGFYRK 60

RESULT 12  
 US-09-249-473-59  
 Sequence 59, Application US/09249473

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 APPLICANT: Stanssens, Patrick Eric Hugo  
 APPLICANT: Messens, Joris Hilda Lieven  
 APPLICANT: Lauwersreys, Marc Joseph  
 APPLICANT: Laroche, Yves Rene  
 APPLICANT: Jespers, Laurent Stephane  
 APPLICANT: Gansmans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew W.  
 APPLICANT: Bergman, Peter W.  
 TITLE OF INVENTION: NEMATOIDE-EXTRACTED SERINE PROTEASE  
 INHIBITORS AND ANTICOAGULANT  
 TITLE OF INVENTION: PROTEIN  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Dyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0

RESULT 13  
 US-08-249-473-59  
 Sequence 59, Application US/08465380

GENERAL INFORMATION:  
 APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
 APPLICANT: Joris H.L. Mensens, Marc J. Lauwersreys,  
 APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
 APPLICANT: Yannick G.J. Gansmans, Matthew Moyle,  
 APPLICANT: Peter W. Bergman  
 TITLE OF INVENTION: NEMATOIDE-EXTRACTED ANTICOAGULANT  
 TITLE OF INVENTION: PROTEIN  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: Storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/465,380  
 FILING DATE: June 5, 1995  
 CLASSIFICATION: 530  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/326,110  
 REFERENCE/DOCKET NUMBER: 213/268  
 TELECOMMUNICATION INFORMATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 FILING DATE: October 18, 1994  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 128:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 91 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 ORGANISM: Ancylostoma caninum  
 US-08-465-380-128

Query Match 1 KATMOCGENEKYDSCGSKCDKCKYDGVEEDDEEPNPLVRYCHODCVCEEGFYRNRK 60  
 Best Local Similarity 100.0%; Score 486; DB 2; Length 91;  
 Matches 84; Conservatve 0; Indels 0; Gaps 0;

RESULT 15  
 US-08-486-397-128  
 Sequence 128, Application US/08486397  
 ; Patent No. 5866512  
 ; GENERAL INFORMATION:  
 ; APPLICANT: George P. Vlasuk, Patrik H. Stanssens,  
 ; ADDRESS: Joris H.L. Mensens, Marc J. Lauwersys,  
 ; APPLICANT: Yves R. Laroché, Laurent S. Jespers,  
 ; APPLICANT: Yannick G.J. Gaussemans, Matthew Moyle,  
 ; APPLICANT: Peter W. Bergum  
 ; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
 ; TITLE OF INVENTION: PROTEIN  
 ; NUMBER OF SEQUENCES: 357  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/486,397  
 ; FILING DATE: June 5, 1995  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3 5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FASSEQ Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/480,478

NUMBER OF SEQUENCES: 86  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3 5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FASSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/480,478

Query Match 1 KATMOCGENEKYDSCGSKCDKCKYDGVEEDDEEPNPLVRYCHODCVCEEGFYRNRK 60  
 Best Local Similarity 100.0%; Score 486; DB 2; Length 91;  
 Matches 84; Conservatve 0; Indels 0; Gaps 0;

RESULT 15  
 US-08-486-397-128  
 Sequence 128, Application US/08486397  
 ; Patent No. 5866512  
 ; GENERAL INFORMATION:  
 ; APPLICANT: George P. Vlasuk, Patrik H. Stanssens,  
 ; ADDRESS: Joris H.L. Mensens, Marc J. Lauwersys,  
 ; APPLICANT: Yves R. Laroché, Laurent S. Jespers,  
 ; APPLICANT: Yannick G.J. Gaussemans, Matthew Moyle,  
 ; APPLICANT: Peter W. Bergum  
 ; TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
 ; TITLE OF INVENTION: PROTEIN  
 ; NUMBER OF SEQUENCES: 357  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/486,397  
 ; FILING DATE: June 5, 1995  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3 5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: FASSEQ Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/480,478

NUMBER OF SEQUENCES: 86  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3 5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: FASSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/480,478

TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 128:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 91 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma caninum  
US-08-486-397-128

Query Match      100.0%;    Score 486;    DB 2;    Length 91;  
Best Local Similarity    100.0%;    Pred. No. 5.1e-43;  
Matches    84;    Conservative 0;    Mismatches 0;    Indels 0;    Gaps 0;

Qy	1 KATMQCGNEKVDSCGSBEGSKYDVEEEDEEENPCLVRCHQDCVCEEGYRANK 60
Db	8 KATMQCGNEKVDSCGSBEGSKYDVEEEDEEENPCLVRCHQDCVCEEGYRANK 67

Qy      61 DDKCVSAEDCELDDNMDFTYPGTRN 84  
Db      68 DDKCVSAEDCELDDNMDFTYPGTRN 91

Search completed: September 24, 2004, 07:50:00  
Job time : 53.1684 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 24, 2004, 07:35:06 ; Search time 723.284 Seconds  
 (without alignments)  
 37.345 Million cell updates/sec

Title: US-09-498-556C-59

Perfect score: 486

Sequence: 1 KATNQCGENEKYDCGSKEC.....VSAEDCELDNNMDFIYPGTRN 84

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaas/us07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/1/pubpaas/fct\_new\_pub.pep:\*

3: /cgn2\_6/ptodata/1/pubpaas/us06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/1/pubpaas/us06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pubpaas/us07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/1/pubpaas/PCTUS\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/1/pubpaas/us08\_PUBCOMB.pep:\*

8: /cgn2\_6/ptodata/1/pubpaas/us08\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pubpaas/us09A\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pubpaas/us07\_NEW\_PUB.pep:\*

11: /cgn2\_6/ptodata/1/pubpaas/us09C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pubpaas/us09\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/1/pubpaas/us10A\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pubpaas/us10B\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/1/pubpaas/us10C\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/1/pubpaas/us10c\_NEW\_PUB.pep:\*

17: /cgn2\_6/ptodata/1/pubpaas/us60\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/1/pubpaas/us60\_PUBCOMB.pep:\*

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	Sequence 59, App1	486	100.0	84	10	US-09-498-272-59
2	Sequence 128, App1	486	100.0	91	10	US-09-498-272-128
3	Sequence 25, App1	43.6	43.6	82	10	US-09-498-272-25
4	Sequence 49, App1	212	43.6	82	10	US-09-498-272-49
5	Sequence 62, App1	212	43.6	171	10	US-09-498-272-62
6	Sequence 46, App1	202	41.6	86	10	US-09-498-272-46
7	Sequence 48, App1	201	41.4	89	10	US-09-498-272-48
8	Sequence 24, App1	201	41.4	108	10	US-09-498-272-24
9	Sequence 45, App1	199	40.9	86	10	US-09-498-272-45
10	Sequence 43, App1	197.5	40.6	88	10	US-09-498-272-43
11	Sequence 63, App1	195.5	40.2	84	10	US-09-498-272-50
12	Sequence 51, App1	195.5	40.2	162	10	US-09-498-272-63
13	Sequence 64, App1	193.5	39.8	84	10	US-09-498-272-51
14	Sequence 52, App1	191.5	39.8	162	10	US-09-498-272-64
15	Sequence 52, App1	186	38.3	83	10	US-09-498-272-52

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1  
 US-09-498-272-59  
 Sequence 59, Application US-09498272  
 Publication No. US20040113890A1  
 GENERAL INFORMATION:  
 / APPLICANT: Vlaasen, George Phillip  
 Stassens, Patrick Eric Hugo  
 Messens, Joris Hilda Lieven  
 Lauwers, Marc Josef  
 Laroche, Yves Rene  
 Jaspers, Laurent Stephane  
 Gansmans, Yannick Georges Jozef  
 Moyle, Matthew  
 Bergum, Peter W.

TITLE OF INVENTION: NEURODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT

PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: 633 West 47th Street  
 SUITE: 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C., DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 FILING DATE: 04-Feb-2000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995

#### ALIGNMENTS

APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINATIONAL SOURCE:  
 ORGANISM: Ancylostoma caninum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
 US-09-498-272-59

Query Match 100.0%; Score 486; DB 10; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-41;  
 Matches 84; Conservative 0; Mismatches 0; Gaps 0;

Db 1 KATNQGENEKYDCKSGSKCDKCKYDGVEEDDEEPPVCLVRVHQDVCBEGFRNK 60  
 Db 1 KATNQGENEKYDCKSGSKCDKCKYDGVEEDDEEPPVCLVRVHQDVCBEGFRNK 60

RESULT 2  
 US-09-498-272-128  
 Sequence 128, Application US/09498272  
 Publication No. US20030113890A1

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 Stranssens, Patrick Eric Hugo  
 Meessens, Joris Hilda Lieven  
 Lauwers, Marc Josef  
 Laroché, Yves René  
 Jespers, Laurent Stéphane  
 Ganssmans, Yannick Georges Jozef  
 Moyse, Matthew W.  
 Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT

NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEES: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 Storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498,272  
 FILING DATE: 04-Feb-2000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US05/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 128:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 91 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 128:  
 US-09-498-272-128

Query Match 100.0%; Score 486; DB 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-41;  
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KATNQGENEKYDCKSGSKCDKCKYDGVEEDDEEPPVCLVRVHQDVCBEGFRNK 60  
 Qy 1 KATNQGENEKYDCKSGSKCDKCKYDGVEEDDEEPPVCLVRVHQDVCBEGFRNK 60  
 Db 8 KATNQGENEKYDCKSGSKCDKCKYDGVEEDDEEPPVCLVRVHQDVCBEGFRNK 67

RESULT 3  
 US-09-498-272-25  
 Sequence 25, Application US/09498272  
 Publication No. US20030113890A1

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 Stranssens, Patrick Eric Hugo  
 Meessens, Joris Hilda Lieven  
 Lauwers, Marc Josef  
 Laroché, Yves René  
 Jespers, Laurent Stéphane  
 Ganssmans, Yannick Georges Jozef  
 Moyse, Matthew W.  
 Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT

NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEES: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 Storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0

NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT

COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498,272  
 FILING DATE: US/09/498,272  
 FILING DATE: 04-Feb-2000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/113231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 82 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Anyclostoma ceylanicum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
 US-09-498-272-25

Query Match 43.6%; Score 212; DB 10; Length 82;  
 Best Local Similarity 50.0%; Pred. No. 5.3e-14;  
 Matches 38; Conservative 11; Mismatches 19; Indels 8; Gaps 3;

Qy 6 CGENEKYDSCGS-KECDCRCKYDGVEEFDDEEPNVPCLVRVHQD--CVCEBEGFYRNKDD 62  
 Db 4 CGSNEYSDGNDKQCERKCNEDDYEKGDE----ACRSHVCERPGACVCDGFIRNKG 58

Qy 63 KCVSAEDCBLDNMDFI 78  
 Db 59 SCVSESDDCYDNNMDFI 74

RESULT 4  
 US-09-498-272-49  
 Sequence 49, Application US/09498272  
 Publication No. US20030113890A1

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 Stanssens, Patrick Eric Hugo  
 Messens, Joris Hilda Lieven  
 Lauwers, Marc Josef  
 Laroche, Yves Rene  
 Jespers, Laurent Stephane  
 Gansmans, Yannick Georges Jozef  
 Moyle, Matthew W.  
 Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN

NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 400  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498,272  
 FILING DATE: 04-Feb-2000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/113231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 49:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 82 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Anyclostoma ceylanicum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 49:  
 US-09-498-272-49

Query Match 43.6%; Score 212; DB 10; Length 82;  
 Best Local Similarity 50.0%; Pred. No. 5.3e-14;  
 Matches 38; Conservative 11; Mismatches 19; Indels 8; Gaps 3;

Qy 6 CGENEKYDSCGS-KEDCDRCKYDGVEEFDDEEPNVPCLVRVHQD--CVCEBEGFYRNKDD 62  
 Db 4 CGSNEYSDGNDKQCERKCNEDDYEKGDE----ACRSHVCERPGACVCDGFIRNKG 58

Qy 63 KCVSAEDCBLDNMDFI 78  
 Db 59 SCVSESDDCYDNNMDFI 74

RESULT 5  
 US-09-498-272-62  
 Sequence 62, Application US/09498272  
 Publication No. US20030113890A1

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 Stanssens, Patrick Eric Hugo  
 Messens, Joris Hilda Lieven  
 Lauwers, Marc Josef  
 Laroche, Yves Rene  
 Jespers, Laurent Stephane  
 Gansmans, Yannick Georges Jozef  
 Moyle, Matthew W.  
 Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN

Jespers, Laurent Stephane  
Gaussemans, Yannick Georges Jozef  
Moyle, Matthew

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth street  
Suite 4700

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90011

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/498,272

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REGISTRATION DOCKET NUMBER: 216/270

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 171 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

ORIGINAL SOURCE:

.ORGANISM: Ancylostoma ceylanicum

SEQUENCE DESCRIPTION: SEQ ID NO: 62:

US-09-498-272-62

Query Match Score 212; DB 10; Length 171;

Best Local Similarity 50.0%; Pred. No. 1..1e-13;

Matches 38; Conservative 11; Mismatches 19;

Indels 8; Gaps 3;

Length 86;

Query Match Score 202; DB 10;

Best Local Similarity 56.13%; Pred. No. 5..6e-13;

Matches 37; Conservative 15; Mismatches 22;

Indels 4; Gaps 2;

Length 86;

Query Match Score 41.6%;

Best Local Similarity 47.4%; Pred. No. 5..6e-13;

Matches 37; Conservative 15; Mismatches 15;

Indels 4; Gaps 2;

Length 86;

Query Match Score 5 QCGENEKYDSCSGSKCCKKCKYDGVEBEDD-EEPNPVCLVRVCHQ-

DB 93 CGSNEYSDCGNDKQCRKCNEDDYERGDE----ACRSVYCAVCECDGPFYRNGK 147

Query Match Score 6 KCCPGERELDCANKKPCPKKIEETSEBDDDVEETVRCVLRVCLVRCPKCKDGYRNK 64

DB 148 SCVYEDDCEYDNDFI 163

Query Match Score 6 RESULT 6 Sequence 46, Application US/09498272-46

US-09-498-272-46

Publication No. US20030113890A1  
GENERAL INFORMATION:  
APPLICANT: Vlasuk, George Phillip  
Stanssens, Patrick Eric Hugo  
Laureyts, Marc Josef  
Messens, Joris Hilda Lieven  
Laroche, Yves Rene  
Gaussemans, Yannick Georges Jozef  
Moyle, Matthew

TITLE OF INVENTION: NEMATODE EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT

PROTEIN  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90011

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,272  
FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REGISTRATION DOCKET NUMBER: 216/270

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 62:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 171 amino acids  
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

ORIGINAL SOURCE:

.ORGANISM: Ancylostoma ceylanicum

SEQUENCE DESCRIPTION: SEQ ID NO: 62:  
US-09-498-272-62

Query Match Score 212; DB 10; Length 171;  
Best Local Similarity 50.0%; Pred. No. 1..1e-13;  
Matches 38; Conservative 11; Mismatches 19;  
Indels 8; Gaps 3;  
Length 86;

Query Match Score 202; DB 10;  
Best Local Similarity 56.13%; Pred. No. 5..6e-13;  
Matches 37; Conservative 15; Mismatches 22;  
Indels 4; Gaps 2;

Query Match Score 41.6%;  
Best Local Similarity 47.4%; Pred. No. 5..6e-13;  
Matches 37; Conservative 15; Mismatches 15;  
Indels 4; Gaps 2;

Query Match Score 5 QCGENEKYDSCSGSKCCKKCKYDGVEBEDD-EEPNPVCLVRVCHQ-

DB 93 CGSNEYSDCGNDKQCRKCNEDDYERGDE----ACRSVYCAVCECDGPFYRNGK 147

Query Match Score 6 KCCPGERELDCANKKPCPKKIEETSEBDDDVEETVRCVLRVCLVRCPKCKDGYRNK 64

Query Match Score 6 RESULT 6 Sequence 46, Application US/09498272-46

US-09-498-272-46

RESULT 7  
 US-09-498-272-48  
 / Sequence 48, Application US/09498272  
 / Publication No. US20030113890A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Vlasuk, George Phillip  
 Stanssens, Patrick Eric Hugo  
 Mossens, Joris Hilda Lieven  
 Lauwersys, Marc Josef  
 Laroche, Yves Rene  
 Jespers, Laurent Stephane  
 Ganssemans, Yannick Georges Jozef  
 Bergum, Peter W.  
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
 INHIBITORS AND ANTICOAGULANT  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498,272  
 FILING DATE: 04-Feb-000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 48:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 89 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Anencyclotoma ceylanicum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 48:  
 US-09-498-272-48  
 Query Match 41.4%; Score 201; DB 10; Length 89;  
 Best Local Similarity 48.1%; Pred. No. 7.4e-13;

Matches 38; Conservative 13; Mismatches 24; Indexes 4; Gaps 3;  
 Qy 3 TMQQGNEYKVDSCGS-KECDKKCKYDGVEEDDEEPNPFCLVCHQD-CVCBEGFVRN 59  
 / Sequence 24, Application US/09498272  
 / Publication No. US20030113890A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Vlasuk, George Phillip  
 Stanssens, Patrick Eric Hugo  
 Mossens, Joris Hilda Lieven  
 Lauwersys, Marc Josef  
 Laroche, Yves Rene  
 Jespers, Laurent Stephane  
 Ganssemans, Yannick Georges Jozef  
 Moyle, Matthew  
 Bergum, Peter W.  
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
 INHIBITORS AND ANTICOAGULANT  
 PROTEIN  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498,272  
 FILING DATE: 04-Feb-000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 108 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide

ORIGINAL SOURCE: ;  
 ORGANISM: Ancylostoma ceylanicum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
 US-09-498-272-24

Query Match 41.4%; Score 201; DB 10; Length 108;  
 Best Local Similarity 48.1%; Pred. No. 9e-13; Mismatches 24; Indels 4; Gaps 3;  
 Matches 38; Conservative 13; Mismatches 24; Indels 4; Gaps 3;

Qy 3 TMOQGENEYKDSCCS-KEDDKCKYKDGYBEEBDEPNTVPLVVRCHQD-CVCGEGYRNY 59  
 Dbs 26 TNACGLNYYFAECGNNMKCEHRR-BEYNEERDEERTFACILRVCFPRGACTVKDGFYN 84

Qy 60 KDDKCVSADCDLNDMDFI 78  
 Dbs 85 RTGSCVEEDDCYEYENMF 103

RESULT 9  
 sequence 45, Application US/09498272  
 Publication No. US20030113890A1

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 Stanssens, Patrick Eric Hugo  
 Messens, Joris Hilda Lieven  
 Lauwers, Marc Josef  
 Laroche, Yves Rene  
 Jespers, Laurent Stephane  
 Gansmans, Yannick Georges Jozef  
 Moyle, Matthew  
 Bergum, Peter W.

TITLE OF INVENTION: NEMATO-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT

NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 33 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498,272  
 FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEX/FAX: (213) 955-0440

TELE: 67-3510  
 INFORMATION FOR SEQ ID NO: 45:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 86 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 45:  
 US-09-498-272-45

Query Match 40.9%; Score 199; DB 10; Length 86;  
 Best Local Similarity 46.2%; Pred. No. 1.1e-12; Mismatches 22; Indels 4; Gaps 2;

Qy 5 QCGGENEYKDSCCSKECDKKCKYKDGYBEEBDEPNTVPLVVRCHQD-DCVCEEGYRNY 60  
 Dbs 5 KCGPGBLDCANKPKPKCKIETSSBEDDDVDTIVRCLVRVCERPLKCTCKDGTYRNK 64

RESULT 10  
 US-09-498-272-43  
 Sequence 43, Application US/09498272  
 Publication No. US20030113890A1

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 Stanssens, Patrick Eric Hugo  
 Messens, Joris Hilda Lieven  
 Lauwers, Marc Josef  
 Laroche, Yves Rene  
 Jespers, Laurent Stephane  
 Gansmans, Yannick Georges Jozef  
 Moyle, Matthew  
 Bergum, Peter W.

TITLE OF INVENTION: NEMATO-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN

NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498,272  
 FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEX/FAX: (213) 955-0440

FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/LICENET NUMBER: 216/2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 50:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 50  
 US-09-498-272-50

Query Match 40.2%; Score 195.  
 Best Local Similarity 50.0%; Pred. No.  
 Matches 40; Conservative 11; Mismatches 1  
 QY 1 KATMOCGENKYDSOGS-KEDDKCKKVGVY  
 Ddb 1 :||| ||| :||| :||| :||| :|||  
 QY 59 NKDDKCVSAADCEDLDNMDFI 78  
 Db 1 :||| :||| :||| :||| :|||  
 60 NRKGQCYTRDCEYNNMEII 79

RESULT 12  
 US-09-498-272-63  
 i Sequence 63, Application US/09498272  
 i Publication No. US200311390A1  
 GENERAL INFORMATION:  
 APPLICANT: Vlaaruk, George Phillip  
 Stanssens, Patrick Eric  
 Messerey, Joris Hilda Lie  
 Lauwers, Marc Josef  
 Laroché, Yves René  
 Jespers, Laurent Stephan  
 Gansmans, Yannick Georg  
 Moyse, Matthew  
 Bergum, Peter W.  
 TITLE OF INVENTION: NEMATO-EEXTRACT  
 INHIBITORS AND /  
 PROTEIN  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSE: Lyon, Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44MB  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 ADDITIONAL INFORMATION: US/09-498-272-50

PRIORITY APPLICATION DATA:  
 FILING DATE: 04-Feb-2000  
 PCT APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/376,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 63:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 162 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: Peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 63:  
 US-09-498-272-63

Query Match 40.2%; Score 195.5; DB 10; Length 162;  
 Best Local Similarity 50.0%; Pred. No. 4.9e-12;  
 Matches 40; Conservative 11; Mismatches 26; Indels 3; Gaps 3;

Qy 1 KATMOCGNEYKDSGS-KECDKKCKRDGVBEEDDEPPVPLVRC-HQDCVCEBEGYR 58  
 Db 1 KSAKKCGLNEKLQD-CGNLAKACEKKCSDLNEDYKEEDSKRSRECSRVCYCDSEFYR 59

Qy 59 NDDDKCVSAEDCFLDNMDFI 78  
 Db 60 NKKGCQCVTRDCEYDNMFI 79

RESULT 13  
 US-09-498-272-51  
 ; Publication No. US0030113890A1  
 ; Sequence 51, Application US/09498272  
 ; Publication No. US0030113890A1  
 GENERAL INFORMATION:  
 APPLICANT: Viasuk, George Phillip  
 Stanssens, Patrick Eric Hugo  
 Messens, Joris Hilda Lieven  
 Lauroeys, Marc Joseph  
 Larocque, Yves Rene  
 Jespers, Laurent Stephane  
 Gansmans, Yannick Georges Jozef  
 Moyle, Matthew  
 Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN

NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:

STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.

ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
STORAGE

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C., DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/498,272

FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13231

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 216/270

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 64:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: Peptide

ORIGINAL SOURCE:

ORGANISM: Ancylostoma caninum

SEQUENCE DESCRIPTION: SEQ ID NO: 64:

US-09-498-272-64

Bergum, Peter W.  
TITLE OF INVENTION: NEUROTODE-EXTRACTED SERINE PROTEASE  
INHIBITORS AND ANTICOAGULANT  
PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:  
ADDRESSEES: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
Storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C., DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/498,272

FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/13231

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 216/270

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 52:

SEQUENCE CHARACTERISTICS:

LENGTH: 83 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: Ancylostoma duodenale

SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US-09-498-272-52

Query Match 38 3%; Score 186; DB 10; Length 83;  
Best Local Similarity 50.0%; Pred. No. 2.2e-11;  
Matches 40; Conservative 11; Mismatches 25; Indels 4;  
Gaps 4;

Qy 1 KATMOCGENEKYDSDGS-XECDKKCKYDGVEEDDEPNPCLVRVC-HQDCYCEREGFYR 58  
Db 1 KSAKKGCGNLNKLXLD-CGNLKAECKCSDSLNEEDGEEDBKCRSRECIGRVYCDECIFYR 59

Qy 59 NKDDDKCVSAEDCELDNMDFI 78  
Db 60 NKKGQCVTRDCEYDNMEII 79

RESULT 15

US-09-498-272-52

Sequence 52, Application US/09498272  
Publication No. US20030113890A1

GENERAL INFORMATION:

APPLICANT: Vilusuk, George Phillip  
Stanssens, Patrick Eric Hugo  
Messens, Joris Hilda Lieven  
Lauwereys, Marc Joseph  
Laroche, Yves Rene  
Jespers, Laurent Stephane  
Ganssemans, Yannick Georges Jozef  
Moyle, Matthew

Search completed: September 24, 2004, 08:10:03  
Job time: 723.284 secs

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protein = protein search: using SW mode]

run on: September 24, 2004, 07:28:33 ; Search time 51.2842 Seconds

157.555 Million cell updates/sec

perfect score: 486  
title: US-09-498-556C-39  
perfect score: 1  
title: VSAEDCEJNMDFIYPGTRN 84

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Scoring table: BLOSUM62 Gapopen 10 Gapext 0.5

Total number of hits satisfying chosen parameters: 283366

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maximum DB seq length: 200000000

post-processing: Minimum Match

## Lesson 1

+  
1  
0  
D  
F  
F  
F

\* \* \*  
— 1 —

4: *pir4:\**

No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

SUMMARIES

result	Query				Description	
	No.	Score	Match Length	DB ID		
1	125	25.7	561	2 T27318	hypothetical prote	
	2	125	25.7	626	2 T27319	hypothetical prote
	3	113	23.3	490	2 T32003	hypothetical prote
	4	112	23.0	249	2 T24602	hypothetical prote
	5	109.5	22.5	1642	2 T11310	hypothetical prote
	6	105.5	21.7	1456	2 T15088	hypothetical prote
	7	100	20.6	5377	2 T42215	zonadhesin - mouse
	8	99	20.4	1036	2 T17405	scavenger receptor
	9	98.5	20.3	135	2 T15110	hypothetical prote
	10	98	20.2	137	2 T11609	hypothetical prote
	11	96.5	19.9	869	1 JCB858	VLDL receptor prec
	12	95.5	19.7	166	1 H89044	protein B0238_12 [
	13	94.5	19.4	98	2 C89046	protein C10G_4 [1]
	14	94.5	19.4	4660	2 T42237	SP330 protein prec
	15	92.5	19.0	63	2 S07127	chymotrypsin/elast
	16	92.5	19.0	63	2 S08512	chymotrypsin/elast
	17	92.5	19.0	4753	1 A47337	IgD1-receptor-relat
	18	90.5	18.6	195	2 T28803	hypothetical prote
	19	87.7	18.0	802	2 T24293	hypothetical prote
	20	87.5	18.0	949	2 T24294	hypothetical prote
	21	85	17.6	863	1 S51189	VLDL receptor prec
	22	85	17.5	2155	2 T30197	alpha tectorin - m
	23	84.5	17.4	13228	2 T03059	mucin, submaxillary
	24	83	17.1	209	2 T02314	hypothetical prote
	25	82.5	17.0	873	1 A49729	VLDL receptor prec
	26	82.5	17.0	873	1 QRRBTD	VLDL receptor prec
	27	82	16.9	62	2 S35058	trypsin inhibitor
	28	82	16.9	62	2 T30002	hypothetical prote
						-

	Query Match	Best Local Similarity	Score	Pred.	No. 0.00025;	Mismatches	Indices	Gaps	3:
Verbal Communication	25.7%	36.1%	125;	DB 2;	Length 361;				

ALIGNMENTS

1	16.6	16.9	2	T15611
2	16.6	4006	2	T09070
3	16.9	VNHU	1	
4	16.4	3002	2	A47221
5	16.3	548	2	T16612
6	16.3	647	2	A43902
7	16.3	798	2	A28193
8	16.2	1160	2	B8339
9	16.2	1321	2	JB0312
0	16.2	2295	2	C88369
1	16.2	3375	2	T19811
2	16.0	305	2	A46416
3	16.0	78	2	T15884
4	16.0	78	2	T18318
5	16.0	78	2	S52033

RESULT 1  
T27318  
hypothetical protein Y692\_3a - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
ALIGNMENTS

**ALIGNMENTS**  
**RESULT 1**  
T27318      Hypothetical protein Y69H2\_3a - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T27318  
R;McMurry, A.  
submitted to the EMBL Data Library, August 1997  
A;Reference number: Z20343  
A;Accession: T27318  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-561 <WIL>  
A;Cross-references: EMBL:Z98877; PIDN:CAB54472.1; GSPDB:GN00023; CESSP:Y69H2\_3a  
A;Experimental source: clone Y69H2

Query Match 25.7% - Score 125; DB 2; Length 626;  
Best Local Similarity 36.1%; Pred. No. 0.00027;  
Matches 26; Conservative 10; Mismatches 16; Indels 20; Gaps 3;

Qy 5 QCGENEKYDSCGSKECDKKCKYDGVEEDDEEPNVPCLYRVCHQDCVCEBGFYRNKDDKCV  
Db 563 RCRSENEFKFCKTYSQSDTRC-----NEEP-----RFPFQVCTGGCCQEEGFRD 607

Qy 60 KDDKCVSABDCE 71  
Db 608 NSGRKCVTQNDCD 619

RESULT 3  
T32003 hypothetical protein F36H9.4 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999  
C;Accession: T32003  
R;Dante, M.; Kramer, J.; Twyman, B.  
submitted to the EMBL Data Library, July 1997  
A;Description: The sequence of C. elegans cosmid F36H9.  
A;Reference number: Z21110  
A;Accession: T32003  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
A;Residues: 1-490 <DNA>  
A;Cross-references: EMBL:AF016668; PIDN:AAB66095.1; GSPPDB:GN00020; CESP:F36H9.4  
A;Experimental source: strain Bristol N2; clone F36H9  
C;Genetics:  
A;Gene: CESP:F36H9.4  
A;Map position: 2  
A;Introns: 5/3; 22/1; 46/3; 72/3; 199/2; 220/3; 278/3; 306/2; 345/3; 427/3  
A;Length: 626  
A;Mismatches: 2  
A;Indels: 0  
A;Gaps: 0  
Query Match 23.3% - Score 113; DB 2; Length 490;  
Best Local Similarity 34.7%; Pred. No. 0.0029;  
Matches 25; Conservative 9; Mismatches 18; Indels 20; Gaps 4;

Qy 2 ATMOGENEKYDSCGSKECDKKCKYDGVEEDDEEPNVPCLYRVCHQDCVCEBGFYRNKDDKCV  
Db 20 APKCGPNEDFKBCGT-ACEANG-----AECHVMCTMQCTVNCQ---CKDGP 64

Qy 57 YRNKDDKCVSAAE 68  
Db 65 FRNKDKCKCAHVE 76

RESULT 4  
T24604 hypothetical Protein T06E6.10 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
C;Accession: T24604  
R;Mortimore, B.  
submitted to the EMBL Data Library, October 1996  
A;Reference number: Z19911  
A;Accession: T24604  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
A;Map position: 5  
A;Residues: 1-249 <WIL>  
A;Cross-references: EMBL:Z81117; PIDN: CAB03319.1; GSPPDB:GN00023; CESP:T06E6.10  
A;Experimental source: clone T06E6  
A;Gene: CESP:T06E6.10  
A;Introns: 17/1; 54/1; 78/2; 140/1; 164/2; 207/3  
C;Superfamily: ultra-high-sulfur keratin  
C;Genetics:

Query Match 23.0% - Score 112; DB 2; Length 249;  
Best Local Similarity 34.8%; Pred. No. 0.0022;  
Matches 23; Conservative 7; Mismatches 26; Indels 10; Gaps 1;

Qy 6 CGENEKYDSCGSKECDKKCKYDGVEEDDEEPNVPCLYRVCHQDCVCEBGFYRNKDDKCV  
Db 185 CGPNBHIFVGCKNCSDTKC-----NEKRKNCPAVCTFPGCVCLNGFFRDKHDKCV 234

Qy 66 SAEEDC 71  
Db 235 TQEEDC 240

RESULT 5  
T19130 hypothetical protein C09F9.2 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T19130  
R;Shupe, R.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19078  
A;Accession: T19130  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
A;Residues: 1-1642 <WIL>  
A;Cross-references: EMBL:Z81465; PIDN: CAB033861.1; GSPPDB:GN00020; CESP:C09F9.2  
A;Experimental source: clone C09F9  
C;Genetics:  
A;Gene: CESP:C09F9.2  
A;Map Position: 2  
A;Introns: 75/3; 103/2; 220/1; 552/1; 1500/3; 1517/1; 1576/3  
Query Match 22.5% - Score 109.5; DB 2; Length 1642;  
Best Local Similarity 33.8%; Pred. No. 0.016;  
Matches 24; Conservative 11; Mismatches 27; Indels 9; Gaps 3;

Qy 5 QCGENEKYDSCGSKECDKKCKYDGVEEDDEEPNVPCLYRVCHQDCVCEBGFYRNKDDKCV  
Db 319 ECGENEQNSECPSSRECBHSQCDWTHFPEITTNCNSCGTPR-----CICREGFVRMAND 373

Qy 61 DDKCVSAEDECE 71  
Db 374 EDVCPFDRCD 384

RESULT 6  
T15608 hypothetical protein C25E10.7 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C;Accession: T15608  
R;Bradshaw, H.  
submitted to the EMBL Data Library, February 1996  
A;Description: The sequence of C. elegans cosmid C25E10.  
A;Reference number: Z18376  
A;Accession: T15608  
A;Molecule type: DNA  
A;Residues: 1-145 <BR>  
A;Cross-references: EMBL:UE0311; NID:gi1226295; PIDN:AAA92312.1; CESP:C25E10  
A;Experimental source: strain Bristol N2  
C;Genetics:  
A;Gene: CESP:C25E10.7  
A;Introns: 39/3

Query Match 21.7% - Score 105.5; DB 2; Length 145;  
Best Local Similarity 31.8%; Pred. No. 0.0052;  
Matches 21; Conservative 14; Mismatches 20; Indels 11; Gaps 3;

Qy 5 OCGBENKYDSCGSKECDKKCKYDGVEEDDEEPNVPCLYRVCHQDCVCEBGFYRNKDDKCV  
Db 17 ECGKKNQKVACG-YDCEDPQCQCFD-----PTV-SLECKPNACVCKDGYVRNTKND 65

Qy 65 VSAEDC 70  
Db 66 VRLEC 71

**RESULT 7**  
T42215  
zonalessin - mouse  
N;Alternate name: sperm-specific membrane protein  
C;Species: *Mus musculus* (house mouse)  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
C;Accession: T42215  
C;Accession: T42215  
R;Gao, Z.; Garbers, D.L.  
J. Biol. Chem. 273, 3415-3421, 1998  
A;Title: Species diversity in the structure of zonalessin, a sperm-specific membrane protein  
A;Reference number: 222080; PMID: 98123114; PMID: 9452463  
A;Accession: T42215  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: mRNA  
A;Residues: 1-5376 <PRA>  
A;Cross-references: EMBL:U97068; NID:g3327420; PID:93327421; PIDN: AAC26680.1  
C;Genetics:  
A;Gene: Zan  
A;MP Position: 5  
A;Function:  
A;Description: functions in multiple cell adhesion processes  
A;Note: found exclusively on the apical region of the sperm head  
C;Keywords: cell adhesion

Query Match 20.6% Score 100; DB 2; Length 5376;  
Matches 25; Conservative 10; Mismatches 27; Indels 12; Gaps 5;  
RESULT 10  
T15609  
hypothetical protein C25E10.8 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999  
C;Accession: T15609  
R;Bradshaw, H.  
submitted to the EMBL Data Library, February 1996  
A;Description: The sequence of *C. elegans* cosmid C25E10.  
A;Accession: T18376  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
A;Residues: 1-137 <PRA>  
A;Cross-references: EMBL:U50311; NID:g1226295; PID: g1226303; PIDN: AAA92313.1; CESP:C25E1.  
C;Genetics:  
A;Gene: CESP:C25E10.8  
A;Introns: 1/3; 19/1; 42/3  
A;MP Position: 5  
A;Function:  
A;Description: The sequence of *C. elegans* cosmid C25E10.

**RESULT 8**  
T17405  
scavenger receptor cysteine-rich protein precursor - sea urchin (*Strongylocentrotus purpuratus* (purple urchin))  
C;Species: *Strongylocentrotus purpuratus* (purple urchin)  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 11-May-2000  
C;Accession: T17405  
R;Pancer, Z.; Rast, J.P.; Davidson, B.H.  
Immunogenetics 49, 773-786, 1999  
A;Title: Origins of immunity: transcription factors and homologs of effector genes of the immune system  
A;Reference number: 21853; PMID: 9932904; PMID: 1039804  
A;Molecule type: mRNA  
A;Residues: 1-1036 <PAN>  
A;Cross-references: EMBL:AF076513; NID: g94164530; PID: g94164531; PIDN: AAD05493.1  
A;MP Position: 5  
A;Function:  
A;Description: The sequence of *Strongylocentrotus purpuratus* (purple urchin) is highly similar to the sequence of the sea urchin scavenger receptor cysteine-rich protein precursor. The two sequences share a high degree of similarity, particularly in the signal peptide and the first few domains. The sea urchin sequence is longer than the purple urchin sequence by approximately 100 amino acids, which corresponds to the C-terminal domain of the sea urchin protein. The two proteins likely have similar biological functions, such as mediating cellular interactions or responding to environmental stimuli.

Query Match 20.4% Score 99; DB 2; Length 1036;  
Matches 21; Conservative 13; Mismatches 21; Indels 24; Gaps 4;  
RESULT 11  
JC4858  
VLDL receptor precursor - African clawed frog  
N;Alternative names: very low density lipoprotein receptor; vitellogenin receptor  
C;Species: *Xenopus laevis* (African clawed frog)  
C;Date: 14-Aug-1998 #sequence\_revision 14-Aug-1998 #text\_change 16-Jun-2000  
C;Accession: JC4858  
R;Okabayashi, K.; Shoji, H.; Nakamura, T.; Hashimoto, O.; Asashima, M.; Sugino, H.  
Biochem. Biophys. Res. Commun. 224, 406-413, 1996  
A;Title: cDNA cloning and expression of the Xenopus laevis vitellogenin receptor.  
A;Reference number: JC4858; MUID: 9629501; PMID: 8702402  
A;Accession: JC4858

**RESULT 9**  
T15610  
hypothetical protein C25B10.9 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 20-Sep-1999

A;Molecule type: mRNA  
A;Residues: 1-69 <OXA>  
A;Cross-references: GB:AB006906; NID:92366772; PID:BA22145.1; Pred:92366773  
C;Comment: This receptor mediates incorporation of vitellogenin into oocytes.  
C;Superfamily: LDL receptor; EGF homology; LDL receptor ligand-binding repeat homology;  
C;Keywords: duplication; fatty acid metabolism; glycoprotein; receptor; transmembrane  
P:27-869; Product: VLDL receptor #status predicted <STO>  
P:71-793; Domain: extracellular #status predicted <STO>  
P:32-66; Domain: LDL receptor ligand-binding repeat homology <LDL1>  
P:112-148; Domain: LDL receptor ligand-binding repeat homology <LDL2>  
P:153-187; Domain: LDL receptor ligand-binding repeat homology <LDL3>  
P:192-228; Domain: LDL receptor ligand-binding repeat homology <LDL4>  
P:238-272; Domain: LDL receptor ligand-binding repeat homology <LDL5>  
P:277-311; Domain: LDL receptor ligand-binding repeat homology <LDL6>  
P:317-354; Domain: LDL receptor ligand-binding repeat homology <LDL7>  
F:359-393; Domain: EGF homology <EG1>  
F:40-43; Domain: EGF homology <EG2>  
F:440-479; Domain: LDL receptor VWD-containing repeat homology <YW1>  
F:450-525; Domain: LDL receptor VWD-containing repeat homology <YW2>  
F:526-568; Domain: LDL receptor VWD-containing repeat homology <YW3>  
F:569-612; Domain: LDL receptor VWD-containing repeat homology <YW4>  
F:613-655; Domain: LDL receptor VWD-containing repeat homology <YW5>  
F:707-749; Domain: LDL receptor VWD-containing repeat homology <YW6>  
F:794-815; Domain: transmembrane #status predicted <TMM>  
P:816-869; Domain: coated-pit mediated intracellular #status predicted <CYT>  
P:830-834; Region: coated-pit mediated internalization signal  
P:150-203; 777-786; Binding site: carbohydrate (Asn) (covalent) #status predicted  
P:359-370; 365-379; 381-393; 399-409; 405-418; 420-433; 707-720; 716-735; 737-749; Disulfide bond

Query Match Score 96.5%; DB 1; Length 869;  
Best Local Similarity 35.4%; Pred. No. 0.16; Indels 5; Gaps 4;  
Matches 28; Conservative 8; Mismatches 38;

Query Match Score 96.5%; DB 1; Length 869;  
Best Local Similarity 35.4%; Pred. No. 0.16; Indels 5; Gaps 4;  
Matches 28; Conservative 8; Mismatches 38;

2 ATMQGENENKYDSCGSKRCG-DKKCKYDGVEEDEEPNVPCLVRVHQD-CYCEEGFYRN 59  
db 234 APOQCSANHM--PGSGSGEIHKKWRCDGDDADCRDKSDDEINCPSRTCPDQFKCDEDNCNIIH 291

Query Match Score 95.5%; DB 2; Length 165;  
Best Local Similarity 31.4%; Pred. No. 0.049; Indels 11; Gaps 4;  
Matches 22; Conservative 9; Mismatches 28;

1 KATMQQGENENKYDSCGSKKECDKKCKYDGVEEDEDPNVPCLVRVHQDCTCCEBGFYRNK 60  
db 108 QSFQRQRERNETPRTCGS-SCEPSC----ITPRPQACTMOCIVNYC---CSEFVRCP 157

Qy 61 DDRCVSAEDC 70  
Db 158 SG-CVQRDC 166

Qy C89046 protein C10G8.4 [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Accession: C89046  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C;Anonymous: The C. elegans Sequencing Consortium.  
Science 283, 2012-2013, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes, development, behavior and aging  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A;Accession: B89044  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-166 <STO>  
A;Cross-references: GB:chr\_V; PID:AAB65990\_1; PID:92315490; GSPDB:GN00023; CBSP:B0238.1  
C;Genetics:  
A;Gene: B0218.12  
A;Map position: 5

Qy 19.4%; DB 2; Length 98;  
Best Local Similarity 28.8%; Pred. No. 0.039; Indels 27; Gaps 6;

Qy 5 QCGENEKYDSCGSKKECDKKCKYDGVEEDEEPN----VPCLVRVHQDCTCCEBGFYRN 59  
Db 39 RCPSNEEFRSAGT-ACEPRT-----QNPNPQVCTLQCLNVCQ---CSQGTVRG 83

Qy 60 KDDKCVSAEDCFLDNMDFTY 79  
Db 84 PNG-CVPQPQDC-----FVY 96

Qy T42737 T42737 protein precursor - rat  
N;Alternate names: megalin  
C;Species: Rattus norvegicus (Norway rat)  
C;Accession: T42737  
R;Saito, A.; Pietromonaco, S.; Loo, A.K.C.; Farquhar, M.G.  
Proc. Natl. Acad. Sci. U.S.A. 91, 9725-9729, 1994  
A;Title: Complete cloning and sequencing of rat gp330/megalin, a distinctive member of the LDL receptor ligand-binding protein family  
A;Reference number: A56173; MUID:95024033; PMID:7937880  
A;Accession: T42737  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-4660 <SAI>  
A;Cross-references: EMBL:134049; NID:9561852; PID:9561853; PID:AAAS1369.1  
A;Expatriate source: strain Sprague-Dawley; kidney  
C;Superramify: alpha-2-macroglobulin receptor; EGF homology;  
F:1-25/Domain: signal sequence #status Predicted <STIG>  
F:26-4660/Product: gp330 protein #status Predicted <MAT>

Qy 19.4%; DB 2; Length 4660;  
Best Local Similarity 30.0%; Pred. No. 0.96; Indels 35; Gaps 8;

Qy 6 CGENEKYDSC-----GSKRC----IKKCKYDFRNKDK--EDDEEPN----PCLVRV----45  
Db 256 CESNQSHRCYPREWACGSGRATSIKVC--DGVPCPGEDENNNTSGRTCGMVCCSV 313

Qy 46 - - - - - CHQ - - - DCYCEEGFYRNKDK--CVSAEDCEL 72  
Db 314 LNCHYQCHQTGPFGECRPPGHIIINSNDSRICIDFDICQI 353

## RESULT 15

S07127 chymotrypsin/elastase inhibitor - common roundworm

C;Species: Ascaris lumbricoides (common roundworm)

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Jul-1997

C;Accession: S07127 R;Babin, D.R.; Peanasky, R.J.; Goos, S.M.

Arch. Biochem. Biophys. 232, 143-161, 1984

A;Title: The isoinhbitors of chymotrypsin/elastase from *Ascaris lumbricoides*: the prima

A;Reference number: S07127; PMID:84255715; PMID:6564898

A;Accession: S07127 A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-63 &lt;BAB&gt;

C;Superfamily: roundworm trypsin inhibitor

Query Match 19.0% Score 92.5; DB 2; Length 63;

Best Local Similarity 32.8%; Pred. No. 0.042;

Matches 22; Conservatve, 5; Mismatches 27; Indels 13; Gaps 4;

QY 6 CGENEKYDSCCSKBCDKCKYDGVERDDDEPNNPCIVRVCOPDCVCE--EGFYRANKDK 63

Db 5 CGPNEWTCTG--CEMKC---GPDE-----NTPCPLMRRPSCECSPGREMRTNDGK 53

QY 64 CVSABDC 70

Db 54 CIPASOC 60

Search completed: September 24, 2004, 07:36:00  
Job time : 53.2842 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.	I protein - protein search, using sw model	P98092 bombyx mori
on:	September 24, 2004, 07:28:33 ; Search time 29.1789 Seconds (without alignment); 149.899 Million cell updates/sec	P26333 trypanosoma
		P91133 bos taurus
		Q61554 mus musculus
		P47944 homo sapien
		P47945 mus musculus
		P09055 mus musculus
		P10499 ascaris suum
		P98163 drosophila
		P2040 drosophila
		P9134 rat
		OT7416 ranitidine si
		ASPI-ANTIST
		11S-09-498-556C-50

Sequence: VSAEDCELDNMDFIYPGTRN 84  
Source: 1 KATMOCGENEKYDSCGSKEC.....  
ID: 100

Scoring table: BUDM62

searched: 141681 seeds 52070155 residues

total number of hits satisfying chosen parameters.

minimum DB over 1 month: 0

maximum DB seq length: 2000000000

*post-processing:* Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

SwissProt\_42;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

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Result No.	Score	Query	Match	Length	DB	ID	Description
1	117	24.1	CYB6	77	1	PIMHY	Q8t0W0 pimpla hypo
2	110.5	22.7	AMC1	56	1	APIMB	P56682 apis mellif
3	103	21.2	ZAN	2812	1	HUMAN	Q9Y493 homo sapien
4	100.5	20.7	IMPT	170	1	GALME	P82176 galleria me
5	100	20.6	ALL6	71	1	APIMB	P83563 apis mellif
6	100	20.6	ZAN	5376	1	MOUSE	Q8B799 mus musculus
7	94.5	19.4	LRP2	4660	1	RAT	P98158 rattus norv
8	92.5	19.0	ICE1	63	1	ASCSU	P07851 ascaris suu
9	92.5	19.0	LRP	4753	1	CABEL	Q04833 caenorhabdi
10	87.5	18.0	VWF	2813	1	CANEA	P028295 canis famil
11	87	17.9	A625	115	1	DROME	O46202 drosophila
12	86.5	17.8	LRP2	4655	1	HUMAN	P98164 homo sapien
13	85.5	17.6	ICSB2	65	1	ASCSU	P07852 ascaris suu
14	85.5	17.6	LDVR	863	1	CHICK	P98165 gallus gallu
15	82.5	17.0	LDVR	873	1	HUMAN	P98166 homo sapien
16	82.5	17.0	LDVR	873	1	MOUSE	P98166 mus musculu
17	82.5	17.0	LDVR	873	1	RABIT	P35953 oryctolagus c
18	82.5	17.0	LDVR	873	1	RAT	P98166 rattus norv
19	82.5	17.0	ZAN	2282	1	RABIT	P757999 oryctolagus c
20	82	16.9	ITR1	62	1	ASCSU	P19398 ascaris suu
21	81.5	16.8	IXCL1	59	1	BOOMI	P10035 boophilus m
22	81.5	16.8	TENV	1808	1	CHICK	P10039 gallus gallu
23	81	16.7	MT4	62	1	CANPA	Q9tuis canis famil
24	80	16.5	ADJ10	790	1	HUMAN	P04272 homo sapien
25	79.5	16.4	VWF	2813	1	HUMAN	P04275 homo sapien
26	79.5	16.4	PBN1	2871	1	HUMAN	P35555 homo sapien
27	79	16.4	2871	1	PIG	Q9tvt36 sus scrofa	
28	78.5	16.2	ASP2	77	1	ANISI	O77417 anisakis si
29	78.5	16.2	ITB1	798	1	XENILA	P12606 xenopus lae
30	78.5	16.2	WVF	937	1	BOVIN	P12012 bos tauru
31	78.5	16.2	UN52	3375	1	CABEL	Q06561 caenorhabdi
32	78	16.0	TMN5	289	1	MOUSE	P27512 mus musculu

SUBCELLULAR LOCATION: Secreted (Potential membrane inhibitor of constrictive domain)

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**RESULT 2**

AMCI\_APME STANDARD; PRT; 56 AA.  
 ID\_AMCI\_APME  
 AC P56682;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DE Chymotrypsin inhibitor (AMCI).  
 OS Apis mellifera (Honeybee).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
 OC Apidae; Apis.  
 OX NCBI\_TaxID=7460;

[1] RN SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6).  
 RP TISSUE=Testis;  
 RC TISSUE=Testis;  
 RA Cheung T.L., Wassler M.J., Cornwall G.A., Hardy D.M.;  
 RT "Multiple intra-species variants of human zonadhesin.";  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

[2] RN PARTIAL SEQUENCE FROM N.A.  
 RP MEDLINE=99018118; Published=9799793;  
 RX Glöckner G., Scheerer S., Schattdevoy R., Boright A.P., Weber J., Tsui L.-C., Rosenthal A.;  
 RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C., Miller W., Koop B.F.;  
 RT "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CMTL1 loci reveals 17 genes.";  
 RT Genome Res. 8:1060-1073 (1998).  
 RL GenBank Res. 8:1060-1073 (1998).

[3] RN SEQUENCE OF 1810-2812 FROM N.A. (ISOFORM 1).  
 RP MEDLINE=11138439; Published=11239002;  
 RX Wilson M.D., Riemer C., Martindale D.W., Schnuppf P., Boright A.P., RA Cheung T.L., Hardy D.M., Schwartz S., Scherer S.W., Tsui L.-C., Miller W., Koop B.F.;  
 RT "Comparative analysis of the gene-dense ACHE/TFR2 region on human chromosome 7q22 with the orthologous region on mouse chromosome 5.";  
 RT Nucleic Acids Res. 29:1352-1365 (2001).  
 RL GenBank Res. 29:1352-1365 (2001).

[4] RN SEQUENCE OF 2375-2683 FROM N.A. (ISOFORM 7).  
 RP TISSUE=Testis;  
 RX MEDLINE=97271566; Published=9126492;  
 RA Gao Z., Harumi T., Garbers D.L.;  
 RT "Chromosomal localization of the mouse zonadhesin gene and the human zonadhesin gene (ZAN).";  
 RT Genomics 41:119-122 (1997).  
 RL -!- FUNCTION: Binds in a species-specific manner to the zona pellucida of the egg. May be involved in gamete recognition and/or signaling.  
 CC -!- SUBUNIT: Probably forms covalent oligomers.  
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the apical region of the sperm head (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=7;  
 CC Name=3;  
 CC IsoID=Q9Y493-1; Sequence=VSP\_Displayed;  
 CC Name=1;  
 CC IsoID=Q9Y493-2; Sequence=VSP\_001430, VSP\_001431;  
 CC Name=2;  
 CC IsoID=Q9Y493-3; Sequence=VSP\_001428, VSP\_001429;  
 CC Name=4;  
 CC IsoID=Q9Y493-4; Sequence=VSP\_001424, VSP\_001425;  
 CC Name=5;  
 CC IsoID=Q9Y493-5; Sequence=VSP\_001420, VSP\_001421;  
 CC Name=6;  
 CC IsoID=Q9Y493-6; Sequence=VSP\_001422, VSP\_001423;  
 CC Name=7;  
 CC IsoID=Q9Y493-7; Sequence=VSP\_001426, VSP\_001427;  
 CC -!- TISSUE SPECIFICITY: In testis, primarily in haploid spermatids.  
 CC -!- DOMAIN: The NAM domains probably mediate sperm adhesion to the zona pellucida.  
 CC -!- DOMAIN: During sperm migration through the reproductive tract, the mucin-like domain might inhibit inappropriate trapping of spermatozoa or promoting adhesion to the oviductal isthmus.  
 CC -!- DOMAIN: The WFED domain 2 may mediate intestinal mucin MUC21.  
 CC -!- DOMAIN: The WFED domain 2 may mediate intestinal mucin MUC21.  
 CC -!- SIMILARITY: Contains 3 NAM domains.  
 CC -!- SIMILARITY: Contains 4 WFED domains.  
 CC -!- SIMILARITY: Contains 4 EGFLike domain.  
 CC -!- CAUTION: Ref.2 sequence differs from that shown due to transposition of a number of exons.

Query Match 22.7%; Score 110.5; DB 1; Length 56;  
 Best Local Similarity 33.3%; Pred. No. 0.00014;  
 Matches 22; Conservative 8; Mismatches 25; Indels 11; Gaps 2;

Qy 5 QCCBNEKYDSCGSKECDKKVTDGVVEBEDDEPNVPCLVRVCHQDCVCEEFYRKDDKC 64  
 Db 2 ECGNEEVNTCGS-ACAPTC-----AQEKTRICTMOCRIGCQCQBGFLRNAGEAC 50

Qy 65 VSAEDC 70  
 Db 51 VLPENC 56

**RESULT 3**

ZAN\_HUMAN STANDARD; PRT; 2812 AA.  
 ID\_ZAN\_HUMAN  
 AC Q9Y493; Q00218; Q96L88; Q96L89; Q96L90;  
 AC Q9XN9; Q9BZ63; Q9BZ84; Q9BZ85; Q9BZ86; Q9BZ87;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 28-DEC-2003 (Rel. 41, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Zonadhesin precursor.

GN Homo sapiens (Human).  
 OS Homo sapiens (Human).  
 OC Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 NCBI\_TaxID=9606;

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RA Weise C., Bender O., Kopacek P., Huchto F.; "Hemolymph proteins of the greater wax moth, *Galleria mellonella*.";  
 RT Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.  
 RL [2]

RP SEQUENCE OF 57-80 FROM N.A., CHARACTERIZATION, AND GLYCOSYLATION.

RC TISSUE=Insect; SUBCELLULAR LOCATION: Extracellular.

RX MEDLINE=198419971; PubMed=9738891;

RA Wade M., Weise C., Kopacek P., Franke P., Vilciunas A.;  
 RT Purification and characterization of an inducible metalloprotease  
 inhibitor from the hemolymph of greater wax moth larvae, *Galleria mellonella*.";  
 RT [3]

RA Biochem. 255:535-543 (1998).

RN REVISION TO 63, AND MASS SPECTROMETRY.

RA Weise C.,  
 Submitted (JUL-2003) to Swiss-Prot.  
 RL [4]

-!- FUNCTION: Inhibits thermolysin and the metalloprotease of  
 B. pombyxa. No activity on trypsin or cysteineprotease papain.  
 -!- INDUCTION: During humoral immune response. By lipopolysaccharide  
 (LPS). Cleaved (Probable).

-!- PTM: Five disulfide bonds are present. When artificially cleaved  
 by thermolysis between Asn-56 and Ile-57, the two obtained chains  
 (called heavy and light chains) remain linked.

CC -!- MASS SPECTROMETRY: MW=360; METHOD=MALDI.

CC -!- MASS SPECTROMETRY: MW=3677; METHOD=MALDI.

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 or send an email to license@isb-sib.ch).

CC EMBL: A5577749; CBEB12200; Li, -.  
 DR InterPro; IPRO02919; EGF like.  
 DR InterPro; IPRO06249; EGF like.  
 DR PROSITE; PS01186; EGF 2; UNKNOWN 2.  
 DR PROSITE; PS01186; EGF 2; UNKNOWN 2.  
 KW Metalloprotease inhibitor; Signal; Glycoprotein.  
 SIGNAL 1  
 FT CHAIN 20 170 AA; 18758 MW; 1A5B272846AD129A CR064;  
 SQ PROTEIN.  
 FT CHAIN 20 88 IMP1 ALPHA.  
 FT SITE 88 89 CLEAVAGE (PROBABLE).  
 FT CARBOHYD 48 48 N-LINKED (GLCNAC. . .).  
 FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CHAIN 20 170 AA; 18758 MW; 1A5B272846AD129A CR064;

Query Match Score 20.7%; DB 1; Length 170;  
 Best Local Similarity 29.2%; Pred. No. 0\_0041; Gaps 2;  
 Matches 19; Conservative 11; Mismatches 30; Indels 5;

RESULT 6

ZAN\_MOUSE STANDARD; PRT; 5376 AA.

ID ZAN\_MOUSE STANDARD; PRT; 5376 AA.

AC 088799; 008647; AC

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

RA Gao Z.; Garbers D.L.;  
 RT "Species diversity in the structure of zonadhesin, a sperm-specific  
 membrane protein containing multiple cell adhesion molecule-like  
 domains." ;  
 RT J. Biol. Chem. 273:3415-3421(1998).  
 RL [2]

OS Mus musculus (Mouse).  
 OC Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;  
 RX MEDLINE=98123114; PubMed=9452463;

RA Gao Z.; Garbers D.L.;  
 RT "Species diversity in the structure of zonadhesin, a sperm-specific  
 membrane protein containing multiple cell adhesion molecule-like  
 domains." ;  
 RT J. Biol. Chem. 273:3415-3421(1998).  
 RL [2]

OS Apis mellifera (Honeybee).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Apidae; Apis.

NCBI\_TaxID=7460;  
 RN [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Venom.

RX MEDLINE=21242713; PubMed=11344362;

RA Kettner A., Hughes G.J., Frutiger S., Astori M., Roggero M.,  
 Spertini F., Corradin G.;  
 RA "Apis m. 6: a new bee venom allergen." ;  
 PL J. Allergy Clin. Immunol. 107:914-920 (2001).

CC -!- MASS SPECTROMETRY: MW=7190; METHOD=MALDI; RANGE=Isoform 6.01.

CC -!- MASS SPECTROMETRY: MW=7400; METHOD=MALDI; RANGE=Isoform 6.02.

CC -!- MASS SPECTROMETRY: MW=7598; METHOD=MALDI; RANGE=Isoform 6.03.

CC -!- MASS SPECTROMETRY: MW=7808; METHOD=MALDI; RANGE=Isoform 6.04.

CC -!- ALLERGEN: Causes an allergic reaction in human. Binds IgE. This is  
 a venom allergen.

CC -!- MISCELLANEOUS: Four isoforms exist: 6.01, 6.02, 6.03 and 6.04.

CC -!- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.

CC -!- DR InterPro; IPRO02919; TIL\_Cyrich.  
 CC -!- PFam: PF01826; TIL; 1.

CC -!- KW Allergen; Polymorphism.

FT DOMAIN 16 70 TIL.

FT DISUFID 16 50 BY SIMILARITY.

FT DISUFID 25 46 BY SIMILARITY.

FT DISUFID 29 42 BY SIMILARITY.

FT DISUFID 33 70 BY SIMILARITY.

FT DISUFID 52 64 BY SIMILARITY.

FT VARIANT 1 4 MISSING (IN API M 6.01 AND 6.02).

FT VARIANT 71 71 G-> GPL OR GLP (IN API M 6.02 AND 6.04).  
 FT SEQ 7598 MW; D619B9C3EE5886B7 CRC64;

Query Match Score 20.6%; DB 1; Length 71;  
 Best Local Similarity 30.4%; Pred. No. 0\_0019;  
 Matches 21; Conservative 8; Mismatches 24; Indels 16; Gaps 3;

QY 5 QCGENEKYDSCGSXECDKCKYDGVVEEDDEPNV--PCLYVRCHDCVCEBGFYRANKD 61  
 DB 15 KCPSNIBIFSRCGR-C2REFC-----PNNVPKPLCIKAPGCVRLGYLNKK 61

DE Zonadhesin precursor.

QY 62 DKCYSAEDC 70  
 DB 62 KVCYFRSKC 70

RESULT 5

ZAN\_MOUSE STANDARD; PRT; 5376 AA.

ID ZAN\_MOUSE STANDARD; PRT; 5376 AA.

AC 088799; 008647; AC

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

RA Gao Z.; Garbers D.L.;  
 RT "Species diversity in the structure of zonadhesin, a sperm-specific  
 membrane protein containing multiple cell adhesion molecule-like  
 domains." ;  
 RT J. Biol. Chem. 273:3415-3421(1998).  
 RL [2]

OS Mus musculus (Mouse).  
 OC Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Testis;  
 RX MEDLINE=98123114; PubMed=9452463;

RA Gao Z.; Garbers D.L.;  
 RT "Species diversity in the structure of zonadhesin, a sperm-specific  
 membrane protein containing multiple cell adhesion molecule-like  
 domains." ;  
 RT J. Biol. Chem. 273:3415-3421(1998).  
 RL [2]

OS Apis mellifera (Honeybee).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Apidae; Apis.

NCBI\_TaxID=7460;  
 RN [1]

RP SEQUENCE OF 4864-5376 FROM N.A.

RC TISSUE=Testis;

RX MEDLINE:97271566; PubMed=9126492;  
 RA Gao Z.; Harumi T.; Garbers D.L.;  
 RT "Chromosome localization of the mouse zonadhesin gene and the human  
 zonadhesin gene."  
 RT Genomics 41:119-122 (1997).  
 RL -!  
 CC -! - FUNCTION: Birds in a species-specific manner to the zona pellucida  
 of the egg. May be involved in gamete recognition and/or  
 signaling.  
 CC -! - SUBUNIT: Probably forms covalent oligomers.  
 CC -! - SUBCELLULAR LOCATION: Type I membrane protein, exclusively on the  
 apical region of the sperm head.  
 CC -! - TISSUE SPECIFICITY: In testis, primarily in haploid spermatids.  
 CC -! - DOMAIN: The MAM domains probably mediates sperm adhesion to the  
 zona pellucida.  
 CC -! - DOMAIN: During sperm migration through the reproductive tracts,  
 the mucin-like domain might inhibit inappropriate trapping of  
 spermatozoa or promoting adhesion to the oviductal isthmus.  
 CC -! - DOMAIN: The VWF domain 2 may mediate covalent oligomerization (by  
 similarity to human intestinal mucin MUC2).  
 CC -! - SIMILARITY: Contains 3 MAM domains.  
 CC -! - SIMILARITY: Contains 25 VWF domains.  
 CC -! - SIMILARITY: Contains 1 EGF-like domain.

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 or send an email to licensee@isb-sib.ch).

CC EMBL: U97068; AAC226680.1; -.  
 DR EMBL: U83190; AAC53125.1; -.  
 DR PIR: T42215; T42215.  
 DR MGD: MGI:106565; Zan.  
 DR InterPro: IPR0056209; EGF like.  
 DR InterPro: IPR003645; POFN.  
 DR InterPro: IPR006210; IEGF.  
 DR InterPro: IPR000398; MAM domain.  
 DR InterPro: IPR002919; TIL\_Cysrich.  
 DR InterPro: IPR003428; TIL\_Cysrich.  
 DR InterPro: IPR001007; VWF\_C.  
 DR InterPro: IPR001846; VWF\_D.  
 DR PFam: PF006239; MAM; 3.  
 DR PFam: PF01836; TIL; 25.  
 DR PFam: PF02345; TIL; 25.  
 DR PFam: PF00094; vwd; 4.  
 DR SMART: SM00181; EGF; 2.  
 DR SMART: SM00274; EGF; 11.  
 DR SMART: SM00137; MAM; 2.  
 DR SMART: SM00214; WVD; 17.  
 DR SMART: SM00216; WVD; 4.  
 DR PROSITE: PS00022; EGF; 1; 1.  
 DR PROSITE: PS01186; EGF; 2; 18.  
 DR PROSITE: PS0026; EGF; 3; 1.  
 DR PROSITE: PS00740; MAM\_1; FALSE\_NEG.  
 DR PROSITE: PS00060; MAM\_2; 3.  
 KW Signal; Glycoprotein; Transmembrane; EGFR-like domain; Cell adhesion;  
 Repeat

FT SIGNAL 1 17 POTENTIAL.  
 FT CHAIN 18 5376 ZONADHESIN.

FT DOMAIN 18 5310 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 5311 5337 POTENTIAL.  
 FT DOMAIN 5338 5376 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 45 210 MAM 1.  
 FT DOMAIN 215 374 MAM 2.  
 FT DOMAIN 377 542 MAM 3.

FT DOMAIN 547 1170 80 X HEPATAPPETIDE REPEATS (APPROXIMATE)

FT DOMAIN 1171 1280 (NUCIN-LIKE DOMAIN).  
 FT DOMAIN 1281 1669 VWFD 1 (PARTIAL).  
 FT DOMAIN 1670 2055 VWFD 2.  
 FT DOMAIN 2057 2459 VWFD 3.  
 FT DOMAIN 2460 3179 VWFD 4.

FT DOMAIN 2580 2699 VWFD 5 (PARTIAL).  
 FT DOMAIN 2700 2819 VWFD 6 (PARTIAL).  
 FT DOMAIN 2820 2939 VWFD 7 (PARTIAL).  
 FT DOMAIN 2940 3059 VWFD 8 (PARTIAL).  
 FT DOMAIN 3060 3179 VWFD 9 (PARTIAL).  
 FT DOMAIN 3180 3299 VWFD 10 (PARTIAL).  
 FT DOMAIN 3300 3416 VWFD 11 (PARTIAL).  
 FT DOMAIN 3417 3536 VWFD 12 (PARTIAL).  
 FT DOMAIN 3537 3656 VWFD 13 (PARTIAL).  
 FT DOMAIN 3657 3776 VWFD 14 (PARTIAL).  
 FT DOMAIN 3777 3892 VWFD 15 (PARTIAL).  
 FT DOMAIN 3893 4928 VWFD 16 (PARTIAL).  
 FT DOMAIN 4029 4148 VWFD 17 (PARTIAL).  
 FT DOMAIN 4149 4263 VWFD 18 (PARTIAL).  
 FT DOMAIN 4264 4283 VWFD 19 (PARTIAL).  
 FT DOMAIN 4384 4503 VWFD 20 (PARTIAL).  
 FT DOMAIN 4504 4623 VWFD 21 (PARTIAL).  
 FT DOMAIN 4624 4743 VWFD 22 (PARTIAL).  
 FT DOMAIN 4744 4863 VWFD 23 (PARTIAL).  
 FT DOMAIN 4864 5261 VWFD 24 (PARTIAL).  
 FT DOMAIN 5259 5295 VWFD 25.

FT DISULFID 5263 5283 BY SIMILARITY.  
 FT DISULFID 5285 5294 BY SIMILARITY.

CC CARBOHYD 339 339 (POTENTIAL).  
 CC CARBOHYD 499 499 (POTENTIAL).  
 CC CARBOHYD 1216 1216 (POTENTIAL).  
 CC CARBOHYD 1239 1239 (POTENTIAL).  
 CC CARBOHYD 1314 1314 (POTENTIAL).  
 CC CARBOHYD 1814 1814 (POTENTIAL).  
 CC CARBOHYD 1908 1908 (POTENTIAL).  
 CC CARBOHYD 1933 1933 (POTENTIAL).  
 CC CARBOHYD 2038 2028 (POTENTIAL).  
 CC CARBOHYD 2111 2111 (POTENTIAL).  
 CC CARBOHYD 2142 2142 (POTENTIAL).  
 CC CARBOHYD 2332 2332 (POTENTIAL).  
 CC CARBOHYD 2533 2533 (POTENTIAL).  
 CC CARBOHYD 2575 2575 (POTENTIAL).  
 CC CARBOHYD 2662 2692 (POTENTIAL).  
 CC CARBOHYD 2812 2812 (POTENTIAL).  
 CC CARBOHYD 3032 3052 (POTENTIAL).  
 CC CARBOHYD 3065 3065 (POTENTIAL).  
 CC CARBOHYD 3144 3144 (POTENTIAL).  
 CC CARBOHYD 3172 3172 (POTENTIAL).  
 CC CARBOHYD 3288 3288 (POTENTIAL).  
 CC CARBOHYD 3292 3292 (POTENTIAL).  
 CC CARBOHYD 3782 3782 (POTENTIAL).  
 CC CARBOHYD 4005 4005 (POTENTIAL).  
 CC CARBOHYD 4136 4136 (POTENTIAL).  
 CC CARBOHYD 4243 4243 (POTENTIAL).  
 CC CARBOHYD 4254 4254 (POTENTIAL).  
 CC CARBOHYD 4335 4335 (POTENTIAL).  
 CC CARBOHYD 4376 4376 (POTENTIAL).  
 CC CARBOHYD 5136 5136 (POTENTIAL).  
 CC CARBOHYD 5252 5252 (POTENTIAL).  
 SQ SEQUENCE 5376 AA; 579908 MW; OE44DB77DF2A2620 CRC64;

Query Match 20.6%; Score 100; DB 1; Length 5376;  
 Best Local Similarity 33.8%; Prec. No. 0.15;  
 Matches 25; Conservative 10; Mismatches 27; Indexes 12; Gaps 5;

Qy 1 KATMCGENEKYDSCGSKCDKRYDVEEE--DDEBPNVPLCVRVHQDCEVCEGGY 57  
 Db 3412 KITLGCPAHTQYIS-LPSCLPSC--LDPEGGLKDISPKV P - STOKEGCVQCSGYV 3463

58 RNKDKRCVSAEDCE 71  
 3464 LN-SDKCVLRAECD 3476

RESULT 7

LRP2_RAT	STANDARD;	PRT;	4660 AA.	DR	InterPro; IPR00033; Ldl_receptor_rep.
ID P98158;				DR	Pfam; PF00008; EGF_9.
AC P98158;	(Rel. 34, Created)			DR	Pfam; PF00057; LDL_recept_a;
DT 01-OCT-1996	(Rel. 34, Last sequence update)			DR	Pfam; PF00058; LDL_recept_b;
DT 01-OCT-1996	(Rel. 34, Last annotation update)			DR	PRINTS; PR00261; LDLRECEPTOR.
DT 15-MAR-2004	(Rel. 43, Last annotation update)			DR	SMART; SMO0179; EGF_CA; 3.
DE Low-density lipoprotein receptor-related protein 2 precursor (Megalin)				DR	SMART; SMO0135; LY; 34.
DE (Glycoprotein 330) (gp330).				DR	PROSITE; PS00010; ASX_HYDROXYL; 4.
GN LRP2.				DR	PROSITE; PS00022; EGF_1; 1.
OS Rattus norvegicus (Rat).				DR	PROSITE; PS01186; EGF_2; 8.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				DR	PROSITE; PS50026; EGF_3; 8.
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;				DR	PROSITE; PS01187; EGF_CA; 3.
OX NCBI_TaxID=10116;				DR	PROSITE; PS01209; LDLFA_1; 31.
RN [1]	SEQUENCE FROM N.A.			DR	PROSITE; PS50068; LDLFA_2; 36.
RP STRAIN-Sprague-Dawley; TISSUE=Kidney;				KW	Glycoprotein; Repeat; Endopeptidase; Coated pits; Transmembrane; Receptor; EG-like domain; SH3-binding; Signal.
RX MEDLINE-95024033; PubMed=937880;				FT	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED POTENTIAL.
PA Saito A., Pietromonaco S., Loo A.K.C., Farquhar M.G.;				FT	PROTEIN 2.
RT "Complete cloning and sequencing of rat gp330/megalin, a distinctive member of the low density lipoprotein receptor gene family".				FT	EXTRACELLULAR (POTENTIAL).
RT Proc. Natl. Acad. Sci. U.S.A. 91:9725-9729 (1994).				FT	CYTOSPLASMIC (POTENTIAL).
RT				DOMAIN	TRANSMEM.
RP FUNCTION.				FT	DOMAIN
RX MEDLINE-95386696; PubMed=7544804;				FT	DOMAIN
RA Moestrup S.K., Cui S., Vorum H., Bregenbaard C., Bjorn S.E.,				FT	DOMAIN
RA Andres G., Bachinsky D.R., Stamenkovic I., Strickland D.K., Brown D.,				FT	DOMAIN
RA Andres G., McCluskey R.T.;				FT	DOMAIN
RA RT lipoprotein receptor gene family, gp330 and LRP/alpha 2NR, and the distribution in rats of two members of the low-density				FT	DOMAIN
RT receptor-associated protein (RAP). "J. Histochem. Cytochem. 42:541-542 (1994).				FT	DOMAIN
RT -!- FUNCTION: Birds plasminogen, extracellular matrix components, plasminogen activator-plasminogen activator inhibitor type I complex, apolipoprotein E-enriched beta-VLDL, lipoprotein lipase lactoferrin, clusterin and calcium.				FT	DOMAIN
CC -!- FUNCTION: Receptor-mediated uptake of polybasic drugs such as aprotinin, aminoglycosides and polymyxin B.				FT	DOMAIN
CC -!- SUBUNIT: Forms a multimeric complex together with a receptor-associated protein (RAP). Binds to ankyrin-repeat protein 2 (ANKR2) /By similarity/.				FT	DOMAIN
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Expressed in clathrin-coated pits, a soluble form is possibly derived by cleavage at the cell surface.				FT	DOMAIN
CC -!- TISSUE/SPECIFICITY: Epithelial cells of kidney glomerulus and proximal tubule, lung, epidermis, yolk sac, among others.				FT	DOMAIN
CC -!- SIMILARITY: Contains 36 LDL-receptor class A domains.				FT	DOMAIN
CC -!- SIMILARITY: Contains 37 LDL receptor class B domains.				FT	DOMAIN
CC -!- SIMILARITY: Contains 17 EGF-like domains.				FT	DOMAIN
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.ebi.ac.uk/annotation/">http://www.ebi.ac.uk/annotation/</a> or send an email to license@ebi.ac.uk).			FT	DOMAIN
CC	DR PIR0409; AAA51369_1; -.			FT	DOMAIN
CC	DR PIR2737; T42737.			FT	DOMAIN
CC	DR HSP; Q07954; 1CB8.			FT	DOMAIN
CC	DR GlycoSulcDB; P98158; -.			FT	DOMAIN
CC	DR InterPro; IPR000152; Asx_hydroxyl_S.			FT	DOMAIN
CC	DR InterPro; IPR001881; EGF_CA.			FT	DOMAIN
CC	DR InterPro; IPR006209; EGF_like.			FT	DOMAIN
CC	DR InterPro; IPR002172; LDL_receptor_A.			FT	DOMAIN
CC	DR InterPro; IPR006209; EGF_like.			FT	DOMAIN
CC	DR InterPro; IPR002172; LDL_receptor_B.			FT	DOMAIN

FT DOMAIN 2520 2562 LDL-RECEPTOR CLASS B 27.  
 FT DOMAIN 2564 2604 LDL-RECEPTOR CLASS B 28.  
 FT DOMAIN 2605 2647 LDL-RECEPTOR CLASS B 29.  
 FT DOMAIN 2652 2694 EGF-LIKE 10.  
 FT DOMAIN 2699 2739 LDL-RECEPTOR CLASS A 16.  
 FT DOMAIN 2740 2778 LDL-RECEPTOR CLASS A 17.  
 FT DOMAIN 2779 2820 LDL-RECEPTOR CLASS A 18.  
 FT DOMAIN 2821 2862 LDL-RECEPTOR CLASS A 19.  
 FT DOMAIN 2863 2903 LDL-RECEPTOR CLASS A 20.  
 FT DOMAIN 2906 2947 LDL-RECEPTOR CLASS A 21.  
 FT DOMAIN 2948 2992 LDL-RECEPTOR CLASS A 22.  
 FT DOMAIN 2993 3031 LDL-RECEPTOR CLASS A 23.  
 FT DOMAIN 3032 3072 LDL-RECEPTOR CLASS A 24.  
 FT DOMAIN 3075 3112 LDL-RECEPTOR CLASS A 25.  
 FT DOMAIN 3113 3153 EGF-LIKE 11.  
 FT DOMAIN 3154 3194 EGF-LIKE 12. CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 3241 3282 LDL-RECEPTOR CLASS B 23.  
 FT DOMAIN 3284 3333 LDL-RECEPTOR CLASS B 31.  
 FT DOMAIN 3335 3377 LDL-RECEPTOR CLASS B 32.  
 FT DOMAIN 3379 3420 LDL-RECEPTOR CLASS B 33.  
 FT DOMAIN 3421 3461 LDL-RECEPTOR CLASS B 34.  
 FT DOMAIN 3467 3511 EGF-LIKE 13.  
 FT DOMAIN 3512 3552 LDL-RECEPTOR CLASS A 26.  
 FT DOMAIN 3553 3593 LDL-RECEPTOR CLASS A 27.  
 FT DOMAIN 3594 3634 LDL-RECEPTOR CLASS A 28.  
 FT DOMAIN 3635 3675 LDL-RECEPTOR CLASS A 29.  
 FT DOMAIN 3678 3718 LDL-RECEPTOR CLASS A 30.  
 FT DOMAIN 3719 3759 LDL-RECEPTOR CLASS A 31.  
 FT DOMAIN 3759 3797 LDL-RECEPTOR CLASS A 32.  
 FT DOMAIN 3798 3836 LDL-RECEPTOR CLASS A 33.  
 FT DOMAIN 3842 3882 LDL-RECEPTOR CLASS A 34.  
 FT DOMAIN 3883 3924 LDL-RECEPTOR CLASS A 35.  
 FT DOMAIN 3928 3966 LDL-RECEPTOR CLASS A 36.  
 FT DOMAIN 3968 4008 EGF-LIKE 14.  
 FT DOMAIN 4009 4050 EGF-LIKE 15. CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 4156 4197 LDL-RECEPTOR CLASS B 35.  
 FT DOMAIN 4199 4241 LDL-RECEPTOR CLASS B 36.  
 FT DOMAIN 4244 4284 LDL-RECEPTOR CLASS B 37.  
 FT DOMAIN 4332 4370 EGF-LIKE 16.  
 FT DOMAIN 4379 4413 EGF-LIKE 17.  
 FT SITE 4454 SH3-BINDING (POTENTIAL).  
 FT SITE 4457 SH3-BINDING (POTENTIAL).  
 FT SITE 4463 SH3-BINDING (POTENTIAL).  
 FT SITE 4606 4609 SH2-BINDING (POTENTIAL).  
 FT SITE 4619 4625 SH3-BINDING (POTENTIAL).  
 FT SITE 4624 4630 CELL ATTACHMENT SITE (POTENTIAL).  
 FT SITE 1743 1745 ENDOCYTOSIS SIGNAL (POTENTIAL).  
 FT SITE 4522 4527 ENDOCYTOSIS SIGNAL (POTENTIAL).  
 FT SITE 4601 4606 BY SIMILARITY.  
 FT DISULFID 28 40 BY SIMILARITY.  
 FT DISULFID 35 53 BY SIMILARITY.  
 FT DISULFID 47 62 BY SIMILARITY.  
 FT DISULFID 67 80 BY SIMILARITY.  
 FT DISULFID 74 93 BY SIMILARITY.  
 FT DISULFID 87 103 BY SIMILARITY.  
 FT DISULFID 108 120 BY SIMILARITY.

Query Match 19.4%; Score 94.5; DB 1; Length 4660;  
 Best Local Similarity 30.0%; Pred. No. 0, 44; Indels 35; Gaps 8;

Matches 30; Conservative 11; Mismatches 24; FT TURN 7 8  
 FT STRAND 10 12  
 FT STRAND 15 15

Qy 6 CGENEKYDSC-----GSKEC---DKKCKYDGVEE--EDDEEPNV---PCLVRY-- 45  
 Db 256 CESNQSHERCYPREWAGSGGCISDRVC--DGVPBPCBGDDENNVTSGRTGNGVCSV 313

Qy 46 -----CHQ-----DCVCEEGFYRNRKDK--CVSAEDCEL 72  
 Db 314 LNEYQOQTPFGECRPPGHITNSDSDRTIDFDQI 353

RESULT 8  
 ICB1\_ASCSU STANDARD; PRT; 63 AA.  
 ID ICB1\_ASCSU 077419;  
 AC P07851

Query Match 19.0%; Scozo 92.5; DB 1; Length 63;  
 NCBI\_TaxID=6253;  
 RN [1]\_TaxID=6253;

DT 01-AUG-1988 (Rel. 08, Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Chymotrypsin/elastase isoinhibitor 1 (C/B-1 inhibitor) (ASC/E-1).  
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides) (Nematoda; Chromadorea; Ascaridida; Ascaridoidea; Ascaridae; Ascaris).  
 OC  
 OC  
 RP SEQUENCE:i4255715; PubMed=6564898;  
 RA Babin D.R.; Peanasky R.J.; Goos S.M.;  
 RT "The iso-inhibitors of chymotrypsin/elastase from Ascaris  
 RT lumbricoides: the primary structure";  
 RL Arch. Biochem. Biophys. 232:143-161(1984).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9635450;  
 RA Lu C.C.; Nguyen T.; Morris S.; Hill D.; Sakanari J.A.;  
 RT "Anisakis simplex-mutational bursts in the reactive site centers of  
 serine protease inhibitors from an ascarid nematode.";  
 RL Exp. Parasitol. 89:257-261(1998).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH ELASTASE.  
 RX MEDLINE=5000335; PubMed=7922044;  
 RA Huang K.; Strynadka N.C.; Bernard V.D.; Peanasky R.J.; James M.N.;  
 RT "The molecular structure of the complex of Ascaris  
 chymotrypsin/elastase inhibitor with porcine elastase.";  
 RL Structure 2:679-689(1994).  
 CC -!- FUNCTION: Defend the organism against the host's proteinases.  
 CC -!- SUBCELLULAR LOCATION: Contains 1 TIL (Trypsin inhibitory-like) domain.  
 CC -!- SIMILARITY: Contains 1 TIL (Trypsin inhibitory-like) domain.  
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Best Local Similarity 32.8%; Pred. No. 0.0087;  
 Matches 22; Conservative 5; Mismatches 27; Indels 13; Gaps 6

```

  6 CGENEKYDSCGSKEDKXCKYDGEEDDEENVPCLVRVHQDCVCB-EFGYRNRKDDK 63
  5 CGPNEWYTECIG-CENRK---GPDE-----NTPCPIMCRRPSCESPGRMRRTNDGK 53
  64 CVSAEDC 70
  54 CIPASQC 60

```

SUIT 9

P_CAEEL	LRP CAEEL	STANDARD;	PRT;	4753 AA.
Q04833;				
01-OCT-1996	(Rel. 34, Created)			
01-OCT-1996	(Rel. 34, Last sequence update)			
28-FEB-2003	(Rel. 41, Last annotation update)			
Low-density lipoprotein receptor-related protein precursor (LRP).				
LRP-1 OR F29D11.1.				
Caenorhabditis elegans.				
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae; Rhabditidae; Pelerodina; Caenorhabditis.				
[NCBI_TAXID=6239;				
[1]				
SEQUENCE FROM N.A.				
Wilkinson J.;				
MEDLINE=93281622; PubMed=8506301;				
Yochim J., Greenwald I.;				
"A gene for low density lipoprotein receptor-related protein in the				
nematode <i>Caenorhabditis elegans</i> ".				
Proc. Natl. Acad. Sci. U.S.A. 90:4572-4576 (1993).				
[2]				
SEQUENCE FROM N.A.				
STRAIN=Bristol N2;				
Wilkinson J.;				
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.				
-!- FUNCTION: May act as a receptor for the endocytosis of extracellular ligands such as chylomicron remnants, protease-inhibitor complexes and vitellogenin.				
-!- SUBCELLULAR LOCATION: Type I membrane protein.				
-!- SIMILARITY: Contains 35 LDL-receptor class A domains.				
-!- SIMILARITY: Contains 17 EGF-like domains.				
-----				
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-----				
EMBL; M96150; AAA28105.1; -.				
EMBL; Z73390; CAA98124.1; -.				
PIR; A47437; A47437.				
HSSP; Q07954; ICR8.				
WormPep; F29D11.1; CE05765.				
Intertro; IP00015; isx_hydroxy1_S.				
Intertro; IPR001881; EGF_Ca.				
Intertro; IPR0062209; EGF_Like.				
Intertro; IPR002172; Ldl_receptor_A.				
Intertro; IPR00033; Ldl_receptor_A.				
Pfam; PF00057; ldl_recept_A; 34.				
Pfam; PF00058; ldl_recept_b; 26.				
PRINTS; PRO0261; LDURCEPTOR.				
SMART; SM00179; EGF_Ca; 2.				
SMART; SM00192; Ldl_a; 35.				
SMART; SM00135; Ly; 32.				
PROSITE; PS00010; ASX_HYDROXYL;				6.
PROSITE; PS00022; EGF_1; 1.				
PROSITE; PS01186; EGF_2; 3.				
PROSITE; PS00026; EGF_3; 2.				
PROSITE; PS001187; EGF_CA; 3.				







"Identification of glycoprotein 330 as an endocytic receptor for apolipoprotein J/clusterin."  
RL: J. Biol. Chem. 270:13070-13075 (1995).

-!- FUNCTION: Binds specifically clusterin with high affinity, but also ligands in common with other family members: plasminogen, extracellular matrix components, plasminogen activator-plasminogen activator inhibitor-type I complex, apolipoprotein E-enriched beta-VLDL, lipoprotein lipase, lactoferrin and calcium.

-!- FUNCTION: Receptor mediated uptake of polybasic drugs such as aprotinin, aminoglycosides and polymyxin B (By similarity).

-!- FUNCTION: May participate in regulation of parathyroid-hormone and parathyroid-hormone-related protein release.

-!- SUBUNIT: Forms a multimeric complex together with a receptor-associated protein (RAP). Binds to ankyrin-repeat family A protein (ANKR2) (By similarity).

-!- SUBCELLULAR LOCALIZATION: Type I membrane protein.

-!- TISSUE SPECIFICITY: Absorptive epithelia, including renal proximal tubules.

-!- SIMILARITY: Contains 36 LDL-receptor class A domains.

-!- SIMILARITY: Contains 37 LDL receptor class B domains.

-!- SIMILARITY: Contains 17 EGF-like domains.

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RT	DOMAIN	220	LDL-RECEPTOR CLASS A 6.
RT	FT DOMAIN	264	LDL-RECEPTOR CLASS A 7.
RL: J. Biol. Chem. 270:13070-13075 (1995).	FT DOMAIN	309	EGF-LIKE 1.
CC	FT DOMAIN	348	EGF-LIKE 2.
CC	FT DOMAIN	436	LDL-RECEPTOR CLASS B 1.
CC	FT DOMAIN	477	LDL-RECEPTOR CLASS B 2.
CC	FT DOMAIN	479	LDL-RECEPTOR CLASS B 3.
CC	FT DOMAIN	522	LDL-RECEPTOR CLASS B 3.
CC	FT DOMAIN	567	LDL-RECEPTOR CLASS B 4.
CC	FT DOMAIN	569	LDL-RECEPTOR CLASS B 4.
CC	FT DOMAIN	612	LDL-RECEPTOR CLASS B 4.
CC	FT DOMAIN	613	LDL-RECEPTOR CLASS B 5.
CC	FT DOMAIN	659	EGF-LIKE 3.
CC	FT DOMAIN	705	LDL-RECEPTOR CLASS B 6.
CC	FT DOMAIN	753	LDL-RECEPTOR CLASS B 7.
CC	FT DOMAIN	796	LDL-RECEPTOR CLASS B 8.
CC	FT DOMAIN	838	LDL-RECEPTOR CLASS B 8.
CC	FT DOMAIN	882	LDL-RECEPTOR CLASS B 9.
CC	FT DOMAIN	970	EGF-LIKE 4.
CC	FT DOMAIN	1062	LDL-RECEPTOR CLASS A 8.
CC	FT DOMAIN	1065	LDL-RECEPTOR CLASS A 9.
CC	FT DOMAIN	1103	LDL-RECEPTOR CLASS A 10.
CC	FT DOMAIN	1107	LDL-RECEPTOR CLASS A 11.
CC	FT DOMAIN	1147	LDL-RECEPTOR CLASS A 12.
CC	FT DOMAIN	1186	LDL-RECEPTOR CLASS A 12.
CC	FT DOMAIN	1228	LDL-RECEPTOR CLASS A 13.
CC	FT DOMAIN	1268	LDL-RECEPTOR CLASS A 13.
CC	FT DOMAIN	1307	LDL-RECEPTOR CLASS A 14.
CC	FT DOMAIN	1310	LDL-RECEPTOR CLASS A 15.
CC	FT DOMAIN	1349	EGF-LIKE 5.
CC	FT DOMAIN	1350	LDL-RECEPTOR CLASS B 10.
CC	FT DOMAIN	1389	LDL-RECEPTOR CLASS B 11.
CC	FT DOMAIN	1429	LDL-RECEPTOR CLASS B 11.
CC	FT DOMAIN	1478	LDL-RECEPTOR CLASS B 10.
CC	FT DOMAIN	1521	LDL-RECEPTOR CLASS B 11.
CC	FT DOMAIN	1562	LDL-RECEPTOR CLASS B 11.
CC	FT DOMAIN	1566	LDL-RECEPTOR CLASS B 12.
CC	FT DOMAIN	1610	LDL-RECEPTOR CLASS B 13.
CC	FT DOMAIN	1695	LDL-RECEPTOR CLASS B 14.
CC	FT DOMAIN	1700	EGF-LIKE 7.
CC	FT DOMAIN	1741	LDL-RECEPTOR CLASS B 15.
CC	FT DOMAIN	1790	LDL-RECEPTOR CLASS B 16.
CC	FT DOMAIN	1833	LDL-RECEPTOR CLASS B 16.
CC	FT DOMAIN	1883	LDL-RECEPTOR CLASS B 17.
CC	FT DOMAIN	1929	LDL-RECEPTOR CLASS B 17.
CC	FT DOMAIN	1931	LDL-RECEPTOR CLASS B 18.
CC	FT DOMAIN	1972	LDL-RECEPTOR CLASS B 19.
CC	FT DOMAIN	2018	EGF-LIKE 8.
CC	FT DOMAIN	2107	LDL-RECEPTOR CLASS B 20.
CC	FT DOMAIN	2157	LDL-RECEPTOR CLASS B 21.
CC	FT DOMAIN	2202	LDL-RECEPTOR CLASS B 22.
CC	FT DOMAIN	2246	LDL-RECEPTOR CLASS B 23.
CC	FT DOMAIN	2290	LDL-RECEPTOR CLASS B 24.
CC	FT DOMAIN	2331	EGF-LIKE 9.
CC	FT DOMAIN	2342	LDL-RECEPTOR CLASS B 19.
CC	FT DOMAIN	2383	LDL-RECEPTOR CLASS B 19.
CC	FT DOMAIN	2431	LDL-RECEPTOR CLASS B 20.
CC	FT DOMAIN	2478	LDL-RECEPTOR CLASS B 21.
CC	FT DOMAIN	2519	LDL-RECEPTOR CLASS B 22.
CC	FT DOMAIN	2561	LDL-RECEPTOR CLASS B 23.
CC	FT DOMAIN	2563	LDL-RECEPTOR CLASS B 24.
CC	FT DOMAIN	2604	LDL-RECEPTOR CLASS B 24.
CC	FT DOMAIN	2651	EGF-LIKE 9.
CC	FT DOMAIN	2693	LDL-RECEPTOR CLASS B 25.
CC	FT DOMAIN	2738	LDL-RECEPTOR CLASS B 26.
CC	FT DOMAIN	2739	LDL-RECEPTOR CLASS B 27.
CC	FT DOMAIN	2778	LDL-RECEPTOR CLASS A 18.
CC	FT DOMAIN	2820	LDL-RECEPTOR CLASS A 19.
CC	FT DOMAIN	2861	LDL-RECEPTOR CLASS A 20.
CC	FT DOMAIN	2901	LDL-RECEPTOR CLASS A 21.
CC	FT DOMAIN	2945	LDL-RECEPTOR CLASS A 22.
CC	FT DOMAIN	2996	LDL-RECEPTOR CLASS A 23.
CC	FT DOMAIN	2997	LDL-RECEPTOR CLASS A 23.
CC	FT DOMAIN	3029	LDL-RECEPTOR CLASS A 24.
CC	FT DOMAIN	3030	LDL-RECEPTOR CLASS A 25.
CC	FT DOMAIN	3110	LDL-RECEPTOR CLASS A 25.
CC	FT DOMAIN	3111	EGF-LIKE 11.
CC	FT DOMAIN	3151	LDL-RECEPTOR CLASS A 26.
CC	FT DOMAIN	3152	LDL-RECEPTOR CLASS A 26.
CC	FT DOMAIN	3192	LDL-RECEPTOR CLASS A 26.
CC	FT DOMAIN	3280	LDL-RECEPTOR CLASS B 30.
CC	FT DOMAIN	3282	LDL-RECEPTOR CLASS B 31.
CC	FT DOMAIN	3333	LDL-RECEPTOR CLASS B 32.
CC	FT DOMAIN	3375	LDL-RECEPTOR CLASS B 33.
CC	FT DOMAIN	3418	LDL-RECEPTOR CLASS B 33.
CC	FT DOMAIN	3465	LDL-RECEPTOR CLASS B 34.
CC	FT DOMAIN	3509	EGF-LIKE 13.
CC	FT DOMAIN	3510	LDL-RECEPTOR CLASS A 27.
CC	FT DOMAIN	3591	LDL-RECEPTOR CLASS A 28.
CC	FT DOMAIN	3632	LDL-RECEPTOR CLASS A 29.
CC	FT DOMAIN	3633	LDL-RECEPTOR CLASS A 30.
CC	FT DOMAIN	3676	LDL-RECEPTOR CLASS A 31.
CC	FT DOMAIN	3717	LDL-RECEPTOR CLASS A 31.

PT DOMAIN	3757	3795	LDL-RECEPTOR CLASS A 32.	AC P98165;
FT DOMAIN	3796	3834	LDL-RECEPTOR CLASS A 33.	DT 01-OCT-1996 (Rel. 34, Created)
FT DOMAIN	3840	3880	LDL-RECEPTOR CLASS A 34.	DT 01-OCT-1996 (Rel. 34, Last sequence update)
Query Match	17.8%	Score 96.5 ; DB 1; Length 4655;	DE Very low-density lipoprotein receptor precursor (VLDL receptor)	
Best Local Similarity	26.1%	Pred. No. 2.6 ; Mismatches 30; Indels 21; Gaps 5;	DE (Vitellogenin receptor) (Vtg receptor).	
Matches 23; Conservative 14; DDKC-----DKKC-----KXGIVVEEDDEEPNVPCLVRYCHQD 49		GN VLDLR OR VTGR.		
Qy 6 CGENERYDSGSKSKECDKCKYDGVEEDDEPNVPCLVRYCHQD 49		OS Gallus gallus (Chicken).		
Db 3745 CGDNSDENCAPECTEEBFRCYQQCPSRWCIDNDCGNSDR--DCEMTCPE 3801		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Qy 50 CV-CEEQGYRNKDDKCVSAEPCDLDNND 76		OC Archosauria; Aves; Neognathae; Galliformes;		
Db 3802 YFQCTSGHzCVHSELKCGSADC-LDASD 3828		OC Galulus.		
RESULT 13		NCBI_TaxID=9031;		
ICB2_Ascsu	STANDARD;	PRT;	OX RN	
ID P07852;		[1]	RN SEQUENCE FROM N.A.	
AC P07852;			RN STRAIN=White Leghorn; TISSUE=Ovary;	
DT 01-AUG-1988 (Rel. 08, Created)			RX MEDLINE=95045409; PubMed=7957081;	
DT 01-AUG-1988 (Rel. 08, Last sequence update)			RA Bujo H., Hermann M., Kaderlik M.O., Jacobsen L., Sugawara S.,	
DE 10-OCT-2003 (Rel. 42, Last annotation update)			RA Niimpf J., Yamamoto T., Schneider W.J.; member of the LDL receptor family.;	
OS Chymotrypsin/elastase 2 to 5.			RA Barber D.L., Sanders E.J., Aebersold R., Schneider W.J.; "Chicken oocyte growth is mediated by an eight ligand binding repeat.	
CC Ascaris suum (Pig roundworm) (Ascaris lumbricoides).			RT RL "Chymotrypsin/elastase 2 to 5.	
CC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridoidea;			RT RL "Chicken oocyte growth is mediated by an eight ligand binding repeat.	
CC Ascarididae; Ascaris.			CC In order to be internalized, the receptor-ligand complexes must	
OX NCBI_TaxID=6553;			CC tyrosine phosphorylation of Dab1 and modulation of Tau	
RN SEQUENCE.			CC first cluster into clathrin-coated pits. Binding of Reelin induces	
RX MEDLINE=84255715; PubMed=6564898;			CC tyrosine phosphorylation (By similarity).	
RA Babin D.R., Peanasky R.J., Goos S.M.; elastase from Ascaris			CC -I- SUBCELLULAR LOCATION: Type I membrane protein.	
RT "The iso-inhibitors of chymotrypsin/elastase from Ascaris lumbricoides: the primary structure."; Arch. Biochem. Biophys. 233:143-161 (1984).			CC -I- TISSUE SPECIFICITY: Abundant in oocytes, much less in heart and	
CC -I- FUNCTION: Defend the organism against the host's proteases.			CC skeletal muscle.	
CC -I- SUBCELLULAR LOCATION: Secreted.			CC -I- SIMILARITY: Contains 8 LDL-receptor class A domains.	
CC -I- SIMILARITY: Contains 1 TIL (trypsin inhibitory-like) domain.			CC -I- SIMILARITY: Contains 6 LDL-receptor class B domains.	
DR HSSP; P07851; 1EA1.			CC -I- SIMILARITY: Contains 3 EGF-like domains.	
DR InterPro; IPR002919; TIL_Cysrich.			CC	
KW Serine protease inhibitor.			This SWISS-PROT entry is copyright. It is produced through a collaboration	
PT DOMAIN 4	59	TIL	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	
PT DISULFID 4	37	BY SIMILARITY.	CC the European Bioinformatics Institute. There are no restrictions on its	
PT DISULFID 13	32	BY SIMILARITY.	CC use by non-profit institutions as long as its content is in no way	
PT DISULFID 16	28	BY SIMILARITY.	CC modified and this statement is not removed. Usage by and for commercial/	
PT DISULFID 20	59	BY SIMILARITY.	CC entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>	
PT DISULFID 39	53	BY SIMILARITY.	CC or send an email to license@isb-sib.ch).	
PT ACT SITE 30	31	REACTIVE BOND.	CC	
PT VARIANT 25	25	K->N (IN INHIBITOR 2 AND 4).	This SWISS-PROT entry is copyright. It is produced through a collaboration	
PT VARIANT 40	40	T->S (IN INHIBITOR 2 AND 4).	CC between the Swiss Institute of Bioinformatics and the EMBL outstation -	
PT VARIANT 64	65	MISSING (IN INHIBITOR 2).	CC the European Bioinformatics Institute. There are no restrictions on its	
PT VARIANT 65	65	K->R (IN INHIBITOR 3).	CC use by non-profit institutions as long as its content is in no way	
PT VARIANT 65	65	K->R.	CC modified and this statement is not removed. Usage by and for commercial/	
SEQUENCE 65 AA;	7241 MW;	B4E1CA166EA4BE3 CRC64;	CC entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>	
Query Match	17.6%	Score 85.5 ; DB 1; Length 65;	CC or send an email to license@isb-sib.ch).	
Best Local Similarity	23.4%	Pred. No. 0.042; Mismatches 7; Indels 13; Gaps 3;	CC	
Matches 19; Conservative 28;		DR EMBL; X80207; CAA56505.1; -.		
Qy 6 CGENERYDSGSKSKECDKCKYDGVEEDDEPNVPCLVRYCHQD 63		DR PIR; 951789; S51789.		
Db 4 CGKNEVWTCTGT-CELKC-----QDEKTPCALMCRPPSCTPGRMRRTHDK 52		DR ASSP; P01130; IAUJ.		
Qy 64 CVSADC 70		DR InterPro; IPR000152; Axin hydroxyl_S.		
Db 53 CVPVSEC 59		DR InterPro; IPR001881; EGF_Ca.		
RESULT 14		DR InterPro; IPR006209; EGF_Like.		
LDVR CHICK	STANDARD;	DR SMART; SM00192; LDLR.		
ID LDVR_CHICK	PRT;	DR SMART; SM00135; LY; 5.		
DR PROSITE; PS00010; AX_HYDROXYL; 2.		DR PROSITE; PS00057; Ldl_recept_a; 8.		
DR PROSITE; PS00022; EGF_1; FALSE_NEG.		DR PROSITE; PS00058; Ldl_recept_b; 5.		
DR PROSITE; PS01186; EGF_2; 3.		DR PROSITE; PS50026; EGF_3; 2.		
DR PROSITE; PS50026; EGF_3; 2.		DR PROSITE; PS01187; EGF_CA; 2.		
DR PROSITE; PS01179; EGF_CA; 2.		DR PROSITE; PS01209; LDILA; 1.		
DR PROSITE; PS05066; LDILA; 8.		DR PROSITE; PS05066; LDILA; 8.		
GW GLyccoprotein; VLDL; Cholesterol metabolism; Lipid transport;		KW		



similarity). LOCATION: Type I membrane protein.  
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -|- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=2;  
 CC  
 CC   | IsoId=P98155-1; Sequence=Displayed;  
 CC  
 CC   | Name=Short;  
 CC   | IsoId=p98155-2; Sequence=VSP 004304;  
 CC   | ISSUE SPECIFICITY: ABUNDANT IN HEART AND SKELETAL MUSCLE; ALSO  
 CC   | Ovary and kidney; NOT IN LIVER.  
 CC   | - SIMILARITY: Contains 8 LDL-receptor class A domains.  
 CC   | - SIMILARITY: Contains 6 LDL-receptor class B domains.  
 CC   | - SIMILARITY: Contains 3 EGF-like domains.

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CC  
 EMBL; I20470; AA53684\_1; -  
 DR EMBL; D16532; BAQ03969\_1; -  
 DR EMBL; D16495; BAQ03969\_1; JOINED.  
 DR EMBL; D16508; BAQ03969\_1; JOINED.  
 DR EMBL; D16510; BAQ03969\_1; JOINED.  
 DR EMBL; D16514; BAQ03969\_1; JOINED.  
 DR EMBL; D16516; BAQ03969\_1; JOINED.  
 DR EMBL; D16518; BAQ03969\_1; JOINED.  
 DR EMBL; D16520; BAQ03969\_1; JOINED.  
 DR EMBL; D16522; BAQ03969\_1; JOINED.  
 DR EMBL; D16523; BAQ03969\_1; JOINED.  
 DR EMBL; D16524; BAQ03969\_1; JOINED.  
 DR EMBL; D16525; BAQ03969\_1; JOINED.  
 DR EMBL; D16526; BAQ03969\_1; JOINED.  
 DR EMBL; D16527; BAQ03969\_1; JOINED.  
 DR EMBL; D16528; BAQ03969\_1; JOINED.  
 DR EMBL; D16529; BAQ03969\_1; JOINED.  
 DR EMBL; D16530; BAQ03969\_1; JOINED.  
 DR EMBL; D16531; BAQ03969\_1; JOINED.  
 DR EMBL; D16532; BAQ03969\_1; JOINED.  
 DR EMBL; D16534; BAQ03969\_1; JOINED.  
 DR EMBL; D16535; BAQ03969\_1; JOINED.  
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 DR EMBL; D16537; BAQ03969\_1; JOINED.  
 DR EMBL; D16538; BAQ03969\_1; JOINED.  
 DR EMBL; D16539; BAQ03969\_1; JOINED.  
 DR EMBL; D16540; BAQ03969\_1; JOINED.  
 DR EMBL; D16541; BAQ03969\_1; JOINED.  
 DR EMBL; D16542; BAQ03969\_1; JOINED.  
 DR EMBL; D16543; BAQ03969\_1; JOINED.  
 DR EMBL; D16544; BAQ03969\_1; JOINED.  
 DR EMBL; D16545; BAQ03969\_1; JOINED.  
 DR EMBL; D16546; BAQ03969\_1; JOINED.  
 DR EMBL; D16547; BAQ03969\_1; JOINED.  
 DR EMBL; D16548; BAQ03969\_1; JOINED.  
 DR EMBL; D16549; BAQ03945\_1; -  
 DR EMBL; D16494; BAQ03946\_1; -  
 DR EMBL; D12431; AAA61344\_1; -  
 DR PIR; A49729; A49729.  
 HSSP; P01130; IAUJ.  
 DR Gene; HGNC:12698; VLDLR.  
 MIM; 192977; -  
 DR GO; GO:0005886; C:plasma membrane; TAS.  
 DR GO; GO:0005041; P:low-density lipoprotein receptor activity; TAS.  
 DR GO; GO:0007613; P:memory; TAS.  
 DR GO; GO:0007399; P:neurogenesis; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR000152; Ax<sub>n</sub> hydroxyl\_S.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR006209; EGF\_1-like.  
 DR InterPro; IPR002172; LDL\_receptor\_A.  
 DR InterPro; IPR000033; Ldl\_receptor\_rep.  
 DR Pfam; PF00068; EGF\_2.  
 DR Pfam; PF00057; Ldl\_recept\_a; 8.  
 DR Pfam; PF00058; Ldl\_recept\_b; 5.  
 DR PRINTS; PR00261; LDLRECEPTOR.  
 SMART; SM00179; EGF\_CA; 2.  
 SMART; SM00192; LDIA; 8.  
 SMART; SM00125; LY\_5.  
 PROSITE; PS00010; ASX\_HYDROXYL; 2.  
 PROSITE; PS00022; EGF\_1; FALSE\_NEG.  
 PROSITE; PS01186; EGF\_2; 3.  
 PROSITE; PS50026; EGF\_3; 2.  
 PROSITE; PS01187; EGF\_CA; 1.  
 PROSITE; PS01209; LDLRA\_1; 8.  
 PROSITE; PS50068; LDLRA\_2; 8.

KW	Glycoprotein; VLDL; Cholesterol metabolism; Lipid transport;
KW	Endocytosis; Coated pit; Transmembrane; Receptor; Signal;
KW	EGF-like domain; Repeat; Alternative splicing; Polymorphism.
POTENTIAL,	VERY LOW-DENSITY LIPOPROTEIN RECEPTOR.
POTENTIAL,	EXTRACELLULAR (POTENTIAL).
POTENTIAL,	CYTOSPLASMIC (POTENTIAL).
POTENTIAL,	EXTRACELLULAR (POTENTIAL).
FT SIGNAL	28
FT CHAIN	873
FT DOMAIN	28
FT TRANSMEM	799
FT DOMAIN	873
FT DOMAIN	69
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FT DOMAIN	110
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FT DOMAIN	696
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FT DOMAIN	750
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FT SITE	832
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FT DISULFID	400
FT DISULFID	410
FT DISULFID	419
FT DISULFID	421
FT DISULFID	434
Query Match	17.0%
Best Local Similarity	31.7%
Matches	26;
Conservative	38;
Mismatches	7;
Indels	11;
Gaps	4;
QCGENEKYDS-----CGSKKC-DKKCKYDGVBEDDEPNVCLVRYCHOD-CVCEEE	54
Qy	5
Db	228
Qy	55
Db	288

Search completed: September 24, 2004, 07:34:56

Fri Sep 24 08:54:02 2004

us-09-498-556c-59.sep04.rsp

Page 16

Job time : 31.1789 secs

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post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :
A_Geneseq_29Jan04:*
1: GeneseqP1980s:*
2: GeneseqP1990s:*
3: GeneseqP2000s:*
4: GeneseqP2001s:*
5: GeneseqP2002s:*
6: GeneseqP2003s:*
7: GeneseqP2003s:*
8: GeneseqP2004s:*

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No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
					Aar91721 NAP subse Nematode
1	30	93.8	5	2 AAR91721	Aay30440 Nematode
2	30	93.8	5	2 AAY30440	Aab15325 NAP domai
3	30	93.8	5	3 AAB15325	Aar91730 NAP subse Nematode
4	30	93.8	7	2 AAR91730	Aay30449 Nematode
5	30	93.8	7	2 AAY30449	Aab15334 NAP domai
6	30	93.8	7	3 AAB15334	Aay30420 Nature ne
7	30	93.8	78	2 AAY30420	Aab15305 A. caninu
8	30	93.8	78	3 AAB15305	Aay30422 Nature ne
9	30	93.8	82	2 AAY30422	Aay30399 Nematode
10	30	93.8	82	2 AAY30399	Aab15293 A. ceylan
11	30	93.8	82	3 AAB15293	Aab15307 A. ceylan
12	30	93.8	82	3 AAB15307	Aay30425 Nature ne
13	30	93.8	83	2 AAY30425	Aay30432 Nature ne
14	30	93.8	84	2 AAY30432	Aay30423 Nature ne
15	30	93.8	84	2 AAY30423	Aay30424 Nature ne
16	30	93.8	84	3 AAY30424	Aab15317 A. caninu
17	30	93.8	84	3 AAB15317	Aam91998 Human dig
18	30	93.8	86	4 AAM91998	Aay30421 Nature ne
19	30	93.8	89	2 AAY30421	Aar91701 AcANApoC2.
20	30	93.8	91	2 AAR91701	Aay30393 Nematode
21	30	93.8	91	2 AAY30393	Aay30544 Nematode
22	30	93.8	91	1 AAY30544	Aab15346 A. caninu
23	30	93.8	91	3 AAB15346	Aar91709 AcANApo31.
24	30	93.8	97	2 AAR91709	

ATTACHMENTS

**RESULT 1**  
 AAR91721  
 ID AAR91721 standard; protein; 5 AA.  
 XX  
 AC AAR91721;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 17-NOV-1996 (first entry)  
 XX DE NAP subsequence.  
 XX AC NamNAP; HDPNNP; NamNAP; AcNAP; A  
 XX KW nematode-extracted anticoagulant

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(CORV- ) CORVAS INT INC.

125-APR-1996 ; 95WO-US013231 .

117-OCT-1995 ; 94US-00326110 .

118-OCT-1994 ; 94US-00461955 .

005-JUN-1995 ; 95US-0046330 .

005-JUN-1995 ; 95US-0046330 .

005-JUN-1995 ; 95US-00486397 .

005-JUN-1995 ; 95US-00486399 .

Stanssens PEH, Messens JHL, Lauwereys MJ, Laroche YR ;  
Jespers LS, Gansmans YGU, Moyle N, Bergum PW ;  
WPI, 1996-222007/22 .

Proteins with anticoagulant and/or serine protease inhibitory activity isolated from nematodes and useful to inhibit blood coagulation.

Claim 10 ; Page 144 ; 243pp ; English .

Proteins with anticoagulant and/or serine protease inhibitory activity isolated from nematodes, are useful to inhibit blood coagulation. The proteins can be added to blood collection tubes defining the collection of mammalian plasma. They are also useful to prevent or inhibit thrombosis and may be given alone or in combination with other therapeutic agents. The proteins can serve as

ATTACHMENTS

**RESULT 1**  
 AAR91721  
 ID AAR91721 standard; protein; 5 AA.  
 XX  
 AC AAR91721;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 17-NOV-1996 (first entry)  
 XX DE NAP subsequence.  
 XX AC NamNAP; HDPNNP; NamNAP; AcNAP; A  
 KW nematode-extracted anticoagulant

1. *Georgian* 2. *Armenian* 3. *Georgian* 4. *Armenian* 5. *Georgian* 6. *Armenian*.

(CORV- ) CORVAS INT INC.

125-APR-1996 ; 95WO-US013231 .

117-OCT-1995 ; 94US-00326110 .

118-OCT-1994 ; 94US-00461955 .

005-JUN-1995 ; 95US-0046330 .

005-JUN-1995 ; 95US-0046330 .

005-JUN-1995 ; 95US-00486397 .

005-JUN-1995 ; 95US-00486399 .

Stanssens PEH, Messens JHL, Lauwereys MJ, Laroche YR ;  
Jespers LS, Gansmans YGU, Moyle N, Bergum PW ;  
WPI, 1996-222007/22 .

Proteins with anticoagulant and/or serine protease inhibitory activity isolated from nematodes and useful to inhibit blood coagulation.

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Proteins with anticoagulant and/or serine protease inhibitory activity isolated from nematodes, are useful to inhibit blood coagulation. The proteins can be added to blood collection tubes defining the collection of mammalian plasma. They are also useful to prevent or inhibit thrombosis and may be given alone or in combination with other therapeutic agents. The proteins can serve as

identification of NAP concn. levels in biological fluids, e.g. to detect mammalian infection with a parasitic worm. They can also be used as immunogens in prophylactic and therapeutic vaccines against parasitic worm infection. The proteins may double the clotting time of human plasma in prothrombin time assays when present at 10-50 nMol, and double the clotting time of human plasma in activated partial thrombin time assays when present at 10-100 nMol. The anticoagulant proteins are pref. derived from *Ancylostoma caninum*, *A. ceylanicum*, *A. duodenale*, *Necator americanus* or *Heligmosomoides polygyrus*. The proteins pref. have 2 NAP domains and specifically inhibit the catalytic activity of the factor VIIa/TF complex in the presence of factor Xa or a catalytically inactive factor Xa deriv., do not specifically inhibit prothrombinase. Proteins given in AAR91720 R91732 are preferred subsequences of a generic NAP sequence. (Updated on 25-MAR-2003 to correct PI field.)

Sequence 5 AA;

Query Match 93.8%; Score 30; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7

Db 1 GFYRN 5

RESULT 3  
AAB15325 standard; peptide; 5 AA.  
ID AAB15325;  
AC AC  
XX DT 19-DEC-2000 (first entry)  
XX DE NAP domain fragment #2.  
XX KW Nematode-extracted anticoagulant Protein; NAP domain; blood clotting;  
XX KW canine hookworm; thrombosis; vaccine.  
XX OS Unidentified.  
XX PN US6087487-A.  
XX PD 11-JUL-2000.  
XX PF 12-FEB-1999;  
XX PR 18-OCT-1994;  
XX PR 05-JUN-1995;  
XX PR 05-JUN-1995;  
XX PR 05-JUN-1995;  
XX PR 05-JUN-1995;  
XX PR 17-OCT-1995;  
XX PR 17-APR-1997;  
XX PA (CORV-) CORVAS INT INC.  
XX PI Lauwereys MJ, Stanssens PBH, Jaspers LS, Ganssemans YGJ, Moyle M;  
XX PI Bergum EW, Messens JHU, Laroche YR, Viasuk GP;  
XX DR WPI; 2000-531359/48.

RESULT 2  
AAY30440 standard; peptide; 5 AA.  
ID AAY30440;  
XX DT 15-NOV-1999 (first entry)  
XX DE Nematode extracted anticoagulant protein fragment.  
XX KW Nematode extracted anticoagulant protein; NAP; anticoagulant;  
KW serine protease inhibitor; NAP domain; Factor VIIa/TF.  
XX CS Unidentified.  
XX PN US5955294-A.  
XX PD 21-SEP-1999.  
XX PP 19-APR-1996; 96US-00634641.  
XX PR 18-OCT-1994; 94US-00326110.  
XX PR 05-JUN-1995; 95US-00461965.  
XX PR 05-JUN-1995; 95US-00465380.  
XX PR 05-JUN-1995; 95US-00486391.  
XX PR 05-JUN-1995; 95US-00486392.  
XX PR 05-JUN-1995; 95US-00486393.  
XX PR 05-JUN-1995; 95US-00486399.  
XX PR 17-OCT-1995; 95WO-US013231.  
XX PA (CORV-) CORVAS INT INC.  
XX PI Lauwereys MJ, Stanssens PBH, Jaspers LS, Ganssemans YGJ, Moyle M;  
XX PI Bergum EW, Messens JHU, Laroche YR, Viasuk GP;  
XX DR WPI; 1999-539569/45.

Screening an isolated protein for Nematode-extracted Anticoagulant Protein domains.  
XX Disclosure; Col 151; 197pp; English.  
XX The present sequence represents a nematode extracted anticoagulant protein (NAP) fragment. The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The

method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay; and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.

SQ Sequence 5 AA;  
Query Match 93.8%; Score 30; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7  
Db 1 GFYRN 5

RESULT 3  
AAB15325 standard; peptide; 5 AA.  
ID AAB15325;  
AC AC  
XX DT 19-DEC-2000 (first entry)  
XX DE NAP domain fragment #2.  
XX KW Nematode-extracted anticoagulant Protein; NAP domain; blood clotting;  
XX KW canine hookworm; thrombosis; vaccine.  
XX OS Unidentified.  
XX PN US6087487-A.  
XX PD 11-JUL-2000.  
XX PF 12-FEB-1999;  
XX PR 18-OCT-1994;  
XX PR 05-JUN-1995;  
XX PR 05-JUN-1995;  
XX PR 05-JUN-1995;  
XX PR 05-JUN-1995;  
XX PR 17-OCT-1995;  
XX PR 17-APR-1997;  
XX PA (CORV-) CORVAS INT INC.  
XX PI Lauwereys MJ, Stanssens PBH, Jaspers LS, Ganssemans YGJ, Moyle M;  
XX PI Bergum EW, Messens JHU, Laroche YR, Viasuk GP;  
XX DR WPI; 2000-531359/48.

New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains.  
Claim 3; Col 28; 197pp; English.

XX The present sequence is a fragment of the NAP domain (see AAB15347), which is found in all nematode-extracted anticoagulant proteins (NAPS).  
CC Proteins of this kind have been shown to be effective at preventing blood CC clotting without causing excessive bleeding. They can be used in blood CC collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an CC atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic CC therapy, percutaneous transluminal coronary angioplasty, disseminated

intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes (the coding sequences can also be used for this) or as diagnostic tests. The proteins can also be used as vaccines against nematode parasites.

XX SQ Sequence 5 AA;

Query Match 93.8%; Score 30; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

DB 1 GFYRN 5

RESULT 4  
AAR1730

ID AAR91730 standard; protein; 7 AA.

XX AAR1730;

AC

XX DT 25-MAR-2003 (revised)

DT 17-NOV-1996 (first entry)

XX DE NAP subsequence.

XX FW ACANAP; EPONAP; NamNAP; AcenAP; AduNAP; anticoagulant;

KW nematode-extracted anticoagulant protein; serine protease; nematode;

KW thrombosis; parasitic worm.

XX OS Synthetic.

XX FH Key-Difference 1

FT /label= Glu, ASP, OTHER

FT /note= "at least one of residue 1 or residue 2 is Glu or

FT ASP"

FT Misc-difference 2

FT /label= Glu, ASP, OTHER

FT /note= "at least one of residue 1 or residue 2 is Glu or

FT ASP"

FT XX WO9612021-A2.

XX PD 25-APR-1996.

XX PF 17-OCT-1995; 95WO-US013231.

XX PR 18-OCT-1994; 94US-00326110.

PR 05-JUN-1995; 95US-00461965.

PR 05-JUN-1995; 95US-00465380.

PR 05-JUN-1995; 95US-00485397.

PR 05-JUN-1995; 95US-00486399.

XX PA (CORV-) CORVAS INT INC.

XX PI Vlasuk GP, Stanssens PEH, Messens JHL, Lauwereys MJ, Laroche YR;

PI Jespers LS, Gansmans YGJ, Moyle M, Bergum PW;

XX DR WPI; 1996-222007/22.

XX FT Proteins with anticoagulant and/or serine protease inhibitory activity -

FT isolated from nematodes and useful to inhibit blood coagulation.

XX BS Claim 26; Page 147; 243pp; English.

XX CC Proteins with anticoagulant and/or serine protease inhibitory activity,

CC CC isolated from nematodes, are useful to inhibit blood coagulation. The

CC proteins can be added to blood collection tubes defining the collection

CC of mammalian plasma. They are also useful to prevent or inhibit

CC thrombosis, and may be given alone or in combination with other

therapeutic or in vivo diagnostic agents. The proteins can serve as immunogens to raise antibodies for use in the diagnosis and identification of NAP concn. Levels in biological fluids. They can also be used as mammalian infection with a parasitic worm. The proteins can also be used as vaccines against parasitic infection. The proteins may double the clotting time of human plasma in prothrombin time assays when present at 10-50 nMol, and double the clotting time of human plasma in activated partial thrombin time assays when present at 10-100 nMol. The antiocoagulant proteins are pref. derived from Ancylostoma caninum, A. ceylanicum, A. duodenale, Necator americanus or Heligmosomoides polygyrus. The proteins pref. have 2 NAP domains and specifically inhibit the catalytic activity of the factor VIIa/TF complex in the presence of Factor Xa or a catalytically inactive Factor Xa deriv., do not specifically inhibit prothrombinase. Proteins given in AAR91720-R91732 are preferred subsequences of a generic NAP sequence. (Updated on 25-MAR-2003 to correct PI field.)

XX SQ Sequence 7 AA;

Query Match 93.8%; Score 30; DB 2;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

DB 3 GFYRN 7

RESULT 5  
AY30449

ID AY30449 standard; peptide; 7 AA.

XX AC AY30449;

XX DT 15-NOV-1999 (first entry)

XX DE Nematode extracted anticoagulant protein fragment.

XX KW Nematode extracted anticoagulant protein; NAP; anticoagulant;

KW serine protease inhibitor; NAP domain; factor VIIa/TF.

XX OS Unidentified.

XX PN US5955294-A.

XX PD 21-SEP-1999.

XX PF 19-APR-1996; 96US-00634641.

XX PR 18-OCT-1994; 94US-00326110.

PR 05-JUN-1995; 95US-00461965.

PR 05-JUN-1995; 95US-00465380.

PR 05-JUN-1995; 95US-00485397.

PR 05-JUN-1995; 95US-00486399.

PR 17-OCT-1995; 95WO-US013231.

XX PA (CORV-) CORVAS INT INC.

XX PI Latwerreys MJ, Stanssens PEH, Jespers LS, Gansmans YGJ, Moyle M;

PI Bergum PW, Messens JHL, Laroche YR, Vlasuk GP;

XX DR WPI; 1999-539569/45.

XX PT Screening an isolated protein for Nematode-extracted Anticoagulant Protein domains.

XX PS Disclosure; Col 155; 197pp; English.

XX CC The present sequence represents a nematode extracted anticoagulant protein (NAP) fragment. The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The

CC

CC specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity

XX Sequence 7 AA;

Query Match 93.8%; Score 30; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7

Db 3 GFYRN 7

RESULT 6  
AAB1334  
ID AAB1334 standard; peptide; 7 AA.  
XX  
AC AAB1334;  
XX DT 19-DEC-2000 (first entry)  
XX DE NAP domain fragment #11.  
XX KW Nematode-extracted anticoagulant protein; NAP domain; blood clotting; canine hookworm; thrombosis; vaccine.  
XX OS Unidentified.

FH Key-Value Pairs

FT Misc-difference 1.2  
FT /label= OTHER  
FT /note= "one of these two residues must be either Glu or Asp"  
XX PN US6087487-A.  
XX PD 11-JUL-2000.  
XX PR 12-FEB-1999; 99US-00249451.  
XX PR 18-OCT-1994; 94US-00326110.  
PR 05-JUN-1995; 95US-00461965.  
PR 05-JUN-1995; 95US-00461980.  
PR 05-JUN-1995; 95US-00463397.  
PR 17-OCT-1995; 95US-00486399.  
PR 17-APR-1997; 97US-00809455.  
XX PA (CORV-) CORVAS INT INC.  
XX PT Screening an isolated protein for Nematode-extracted Anticoagulant Protein domains.

PI Lauwers MJ, Stanssens PEH, Jespers LS, Ganssemans YGJ, Moyle M;  
PI Bergum PW, Messens JHL, Laroche YR, Vlasuk GP;  
XX DR WPI; 2000-531359/48.  
XX PT New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains.  
XX PS Claim 4; Col 286; 197pp; English.

CC The present sequence is a fragment of the NAP domain (see AAB13347), which is found in all nematode-extracted anticoagulant proteins (NAPs). Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. They can be used in blood collection tubes to aid the isolation of plasma from the blood, to collect thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes (the coding sequences can also be used for this), or as diagnostic tests. The proteins can also be used as vaccines against nematode parasites

XX SQ Sequence 7 AA;

Query Match 93.8%; Score 30; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7

Db 3 GFYRN 7

RESULT 7  
AAAY30420  
ID AAAY30420 standard; protein; 78 AA.  
XX AC AAAY30420;  
XX DT 15-NOV-1999 (first entry)  
XX DE Mature nematode extracted anticoagulant protein AcaNAP31.  
XX KW Nematode extracted anticoagulant protein; NAP; anticoagulant; serine protease inhibitor; NAP domain; factor VIIa/TF.  
XX OS Ancylostoma caninum.  
XX PN US5955294 A.  
XX PD 21-SEP-1999.  
XX PF 19-APR-1996; 96US-00634641.  
XX PR 18-OCT-1994; 94US-00326110.  
PR 05-JUN-1995; 95US-00441965.  
PR 05-JUN-1995; 95US-0045380.  
PR 05-JUN-1995; 95US-00486397.  
PR 05-JUN-1995; 95US-00486399.  
PR 17-OCT-1995; 95WO-US013231.  
XX PA (CORV-) CORVAS INT INC.  
XX PT Screening an isolated protein for Nematode-extracted Anticoagulant Protein domains.

XX Disclosure; Col 133-134; 197pp; English.  
CC The present sequence represents a nematode extracted anticoagulant and/or serine protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo

activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.

Sequence 78 AA;

Query Match 93.8%; Score 30; DB 2; Length 78;

Best Local Similarity 100.0%; Pred. No. 75; Matches 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7  
DB 54 GFYRN 58

RESULT 8  
AAB15305 standard; protein: 78 AA.  
XX  
AC XX  
DT 06-AUG-2003 (revised)  
DT 19-DEC-2000 (first entry)  
DE A. caninum nematode-extracted anticoagulant protein AcanAP31; 42, 46.  
XX  
Nematode-extracted anticoagulant protein; AcanAP31; AcanAP42; AcanAP46;  
KW canine hookworm; blood clotting; thrombosis; vaccine.  
XX  
OS Ancylostoma caninum.  
XX  
PN US6087487-A.  
XX  
PD 11-JUL-2000.  
XX  
PF 12-FEB-1999; 96US-00249451.  
XX  
PR 18-OCT-1994; 94US-00326110.  
PR 05-JUN-1995; 95US-00461965.  
PR 05-JUN-1995; 95US-00465397.  
PR 05-JUN-1995; 95US-00486397.  
PR 05-JUN-1995; 95US-00486399.  
PR 17-OCT-1995; 95WO-US013231.  
PR 17-APR-1997; 97US-00809455.  
PA (CORV-) CORVAS INT INC.

Lawwerays MJ, Stanssens PEH, Jaspers LS, Ganssemans YGJ, Moyle M;

Bergum PW, Messens JHL, Laroche YR, Viasuk GP;

WPI; 2000-531359/48.

DR N-PSDB; AAA73378.

New cDNA molecule encoding a protein having factor Xa inhibitory activity for preventing and treating blood clotting disorders, comprises nematode-extracted anticoagulant protein domains.

Disclosure; Fig 16; 197pp; English.

The present sequence comprises the Ancylostoma caninum nematode-extracted anticoagulant proteins AcanAP31, AcanAP42 and AcanAP46. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The proteins can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated

intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes (the coding sequence can also be used for this) or as diagnostic tests. The proteins can also be used as a vaccine against nematode parasites. (Updated on 06-AUG-2003 to correct OS field.)

XX  
SQ Sequence 78 AA;

Query Match 93.8%; Score 30; DB 3; Length 78;

Best Local Similarity 100.0%; Pred. No. 75; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7  
DB 54 GFYRN 58

RESULT 9  
AAY30422 standard; protein: 82 AA.  
ID AAY30422;  
XX DT 15-NOV-1999 (first entry)  
XX AAY30422;

Mature nematode extracted anticoagulant protein AcenAP4d2.  
DE XX  
Nematode extracted anticoagulant Protein; NAP; anticoagulant; KW serine protease inhibitor; NAP domain; factor VIIa/TF.  
XX  
OS Ancylostoma ceylanicum.  
XX  
US5955294-A.  
XX  
PD 21-SEP-1999.  
XX  
PF 19-APR-1996; 96US-00624641.  
XX  
PR 18-OCT-1994; 94US-00326110.  
PR 05-JUN-1995; 95US-00461965.  
PR 05-JUN-1995; 95US-00465380.  
PR 05-JUN-1995; 95US-00463997.  
PR 05-JUN-1995; 95US-00463999.  
PR 17-OCT-1995; 95WO-US013231.  
XX  
(CORV-) CORVAS INT INC.

Screening an isolated protein for Nematode-extracted Anticoagulant Protein domains.

Disclosure; Col 135-136; 197pp; English.

The present sequence represents a nematode extracted anticoagulant protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of

CC factor VIIa/TF inhibitory activity. The method is useful for determining  
 CC if a protein has factor VIIa/TF inhibitory activity

XX Sequence 82 AA;

Query Match 93.8%; Score 30; DB 2; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 79;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7  
 Db 51 GFYRN 55

RESULT 1.0

AAV30399 AAV30399 standard; protein; 82 AA.

XX DT 15-NOV-1999 (first entry)

XX DE Nematode extracted anticoagulant protein AcenAP4d2.

XX KW Nematode extracted anticoagulant protein; NAP; anticoagulant;

XX OS serine protease inhibitor; NAP domain; factor VIIa/TF.

XX OS Ancylostoma ceylanicum.

XX PN US5955294-A.

XX PD 21-SEP-1999.

XX PP 19-APR-1996; 96US-00634641.

XX PR 18-OCT-1994; 94US-00326110.

XX PR 05-JUN-1995; 95US-00461965.

XX PR 05-JUN-1995; 95US-00461965.

XX PR 05-JUN-1995; 95US-00465388.

XX PR 05-JUN-1995; 95US-00486397.

XX PR 05-JUN-1995; 95US-00486397.

XX PR 05-JUN-1995; 95US-00486397.

XX PR 05-JUN-1995; 95US-00486397.

XX PR 17-OCT-1995; 95WO-US013231.

XX PR 17-APR-1997; 97US-00809455.

XX PA (CORY-) CORVAS INT INC.

XX PI Lauwereys MJ, Stanssens PEH, Jespers LS, Gansmans YGJ, Moyle M;

XX PI Bergum PW, Messens JHL, Laroche YR, Viasuk GP;

XX DR WPI; 2000-531359/48.

XX PT New cDNA molecule encoding a protein having factor Xa inhibitory activity

XX PT for preventing and treating blood clotting disorders, comprises nematode-

XX PT extracted anticoagulant protein domains.

XX Disclosure; Fig 11; 197pp; English.

XX PS Screening an isolated protein for Nematode-extracted Anticoagulant

XX PT protein domains.

XX Disclosure; Col 111-112; 197pp; English.

CC The present sequence represents a nematode extracted anticoagulant protein (NAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAP domain which has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the activated protein in an ex vivo prothrombin time (PT) assay and an ex vivo activated partial thromboplastin time (aPTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and aPTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PT to aPTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity

XX Sequence 82 AA;

CC Query Match 93.8%; Score 30; DB 3; Length 82;

CC Best Local Similarity 100.0%; Pred. No. 79;

CC Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Sequence 82 AA;

RESULT 13  
 Qy 3 GFYRN 7  
 Db 51 GFYRN 55

RESULT 12  
 AAB15307 ID AAB15307 standard; protein; 82 AA.  
 XX DT 06-AUG-2003 (revised)  
 XX DT 19-DEC-2000 (first entry)

A. ceylanicum nematode-extracted anticoagulant protein: AceNAP4d2 #2  
 XX Nematode-extracted anticoagulant protein: AceNAP4d2; blood clotting  
 KW canine hookworm; thrombosis; vaccine.  
 OS Ancylostoma ceylanicum.  
 XX US6087487-A.  
 PN PD 11-JUL-2000.  
 PR 12-FEB-1999;  
 PR 18-OCT-1994;  
 PR 05-JUN-1995;  
 PR 05-JUN-1995;  
 PR 05-JUN-1995;  
 PR 17-OCT-1995;  
 PR 17-APR-1997;  
 PR 05-JUN-1995;  
 PR 05-JUN-1995;  
 PR 05-JUN-1995;  
 PR 17-OCT-1995;  
 PR 17-APR-1997;  
 PA (CORV-) CORVAS INT INC.  
 PA PI Lauwereys MJ, Stanssens PBH, Jespers LS, Gansmans YGJ, Moyle M;  
 PA PT Bergum PW, Messens JHL, Laroche YR,  
 PA DR WPI: 1999-539569/45.

XX Screening an isolated protein for Nematode-extracted Anticoagulant  
 PT Protein domains.  
 XX Disclosure; Col 137-138; 197pp; English.

CC The present sequence represents a nematode extracted anticoagulant and/or serine  
 CC protease (NAP). The protein has activity as an anticoagulant and/or serine  
 CC protease inhibitor. The protein contains at least one NAP domain which  
 CC has selective inhibitory activity for factor VIIa/TF. The specification  
 CC describes a method for screening an isolated protein at least one domain  
 CC for factor VIIa/TF selective inhibitory activity. The method comprises  
 CC determining the time to clotting effected by a concentration of the  
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo  
 CC activated partial thromboplastin time (aPTT) assay; calculating  
 CC the prolongation of clotting effected by the isolated protein in each of the  
 CC PT and aPTT assay, with respect to a baseline clotting value for each  
 CC assay, where prolongation of clotting is calculated as fold elevation of  
 CC clotting time relative to a baseline clotting value, where a doubling of  
 CC clotting time is deemed a two-fold elevation; and calculating a PT to  
 CC aPTT prolongation ratio, where a ratio at least one is indicative of  
 CC factor VIIa/TF inhibitory activity. The method is useful for determining  
 CC if a protein has factor VIIa/TF inhibitory activity  
 XX Sequence 83 AA;

Query Match 93.8%; Score 30; DB 3; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 79;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 SQ Sequence 82 AA;

RESULT 14  
 Qy 3 GFYRN 7  
 Db 51 GFYRN 55

RESULT 13  
 AAY30425 ID AAY30425 standard; protein; 83 AA.  
 XX AC AAY30425;  
 XX DT 15-NOV-1999 (first entry)  
 XX DS Mature nematode extracted anticoagulant protein; NAP; anticoagulant;  
 KW Nematode extracted anticoagulant protein; NAP domain; Factor VIIa/TF.  
 XX OS Ancylostoma duodenale.  
 XX PN US5955294-A.  
 XX PD 21-SEP-1999.  
 XX PF 19-APR-1996;  
 XX PR 18-OCT-1994;  
 PR 05-JUN-1995;  
 PR 05-JUN-1995;  
 PR 05-JUN-1995;  
 PR 05-JUN-1995;  
 PR 17-OCT-1995;  
 PA (CORV-) CORVAS INT INC.  
 PA PI Lauwereys MJ, Stanssens PBH, Jespers LS, Gansmans YGJ, Moyle M;  
 PA PT Bergum PW, Messens JHL, Laroche YR,  
 PA DR WPI: 1999-539569/45.

XX Disclosure; Col 137-138; 197pp; English.

CC The present sequence represents a nematode extracted anticoagulant and/or serine  
 CC protease (NAP). The protein has activity as an anticoagulant and/or serine  
 CC protease inhibitor. The protein contains at least one NAP domain which  
 CC has selective inhibitory activity for factor VIIa/TF. The specification  
 CC describes a method for screening an isolated protein at least one domain  
 CC for factor VIIa/TF selective inhibitory activity. The method comprises  
 CC determining the time to clotting effected by a concentration of the  
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo  
 CC activated partial thromboplastin time (aPTT) assay; calculating  
 CC the prolongation of clotting effected by the isolated protein in each of the  
 CC PT and aPTT assay, with respect to a baseline clotting value for each  
 CC assay, where prolongation of clotting is calculated as fold elevation of  
 CC clotting time relative to a baseline clotting value, where a doubling of  
 CC clotting time is deemed a two-fold elevation; and calculating a PT to  
 CC aPTT prolongation ratio, where a ratio at least one is indicative of  
 CC factor VIIa/TF inhibitory activity. The method is useful for determining  
 CC if a protein has factor VIIa/TF inhibitory activity  
 XX Sequence 83 AA;

Query Match 93.8%; Score 30; DB 2; Length 83;  
 Best Local Similarity 100.0%; Pred. No. 80;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC	AY34432;	DE	Mature nematode extracted anticoagulant protein AcaNAP45Q1.
XX	XX	XX	
15-NOV-1999	(first entry)	KW	Nematode extracted anticoagulant protein; NAP; anticoagulant;
XX		KW	serine protease inhibitor; NAP domain; factor VIIa/TF.
Mature nematode extracted anticoagulant protein AcaNAPC2.		XX	
XX		OS	Ancylostoma caninum.
KW		XX	
Nematode extracted anticoagulant protein; NAP; anticoagulant;		XX	
XX		XX	serine protease inhibitor; NAP domain; factor VIIa/TF.
OS		OS	Ancylostoma caninum.
XX		XX	
US5955294-A.		PN	
XX		XX	
21-SEP-1999.		PD	
XX		PD	
19-APR-1996;	96US-00634641.	PF	
XX		PF	
18-OCT-1994;	94US-00326110.	PR	
PR		PR	
05-JUN-1995;	95US-00461965.	PR	
PR		PR	
05-JUN-1995;	95US-0045380.	PR	
PR		PR	
05-JUN-1995;	95US-0046397.	PR	
PR		PR	
17-OCT-1995;	95WO-US013231.	XX	
(CORV-) CORVAS INT INC.		PA	
XX		PA	
Lauwersys MJ, Stassens PEH, Jeepers LS, Gansmans YGJ, Moyle M;		PI	
Bergum PW, Messens JHL, Laroche YR, Viasuk GP;		PI	
XX		DR	
XX		WPI; 1999-539569/45.	
XX		PT	
Screening an isolated protein for Nematode-extracted Anticoagulant		PT	
Protein domains.		XX	
(CORV-) CORVAS INT INC.		PS	
XX		CC	
Lauwersys MJ, Stassens PEH, Jeepers LS, Gansmans YGJ, Moyle M;		CC	
Bergum PW, Messens JHL, Laroche YR, Viasuk GP;		CC	
XX		CC	
WPI; 1999-539569/45.		CC	
Screening an isolated protein for Nematode-extracted Anticoagulant		CC	
Protein domains.		CC	
Disclosure; Col 142-144; 197pp; English.		CC	
XX		CC	
The present sequence represents a nematode extracted anticoagulant		CC	
protein (NAP). The protein has activity as an anticoagulant and/or serine		CC	
protease inhibitor. The protein contains at least one NAP domain which		CC	
has selective inhibitory activity for factor VIIa/TF. The specification		CC	
describes a method for screening an isolated protein at least one domain		CC	
for factor VIIa/TF selective inhibitory activity. The method comprises		CC	
determining the time to clotting effected by a concentration of the		CC	
isolated protein in an ex vivo prothrombin time (aPT) assay and an ex vivo		CC	
activated partial thromboplastin time (aPTT) assay; calculating		CC	
prolongation of clotting effected by the isolated protein in each of the		CC	
PT and aPTT assay, with respect to a baseline clotting value for each		CC	
assay, where prolongation of clotting is calculated as fold elevation of		CC	
clotting time relative to a baseline clotting value, where a doubling of		CC	
aPTT prolongation ratio, where a ratio at least one is indicative of		CC	
factor VIIa/TF inhibitory activity. The method is useful for determining		CC	
if a protein has factor VIIa/TF inhibitory activity.		XX	
Sequence 84 AA;		Sequence 84 AA;	
Query Mach		93.8%;	Score 30; DB 2; Length 84;

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: September 24, 2004, 07:28:33 ; Search time 4.27368 Seconds  
(without alignments)  
157.555 Million cell updates/sec

Title: US-09-498-556C-79

Perfect score: 32 Sequence: 1 XXGTYRN 7

Scoring table: BL0SUM62 Gapop 10.0 , Gpext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 Summaries

Database : PIR78:  
1: Pir1:  
2: Pir2:  
3: Pir3:  
4: Pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	30	93.8	77	2	B85684	unknown protein en
2	30	93.8	134	2	S76180	hypothetical prote
3	30	93.8	172	2	S87703	conserved hypothet
4	30	93.8	175	2	S73496	hypoxanthine-guan
5	30	93.8	175	2	P64250	hypoxanthine-guan
6	30	93.8	223	2	AC2302	endonuclease III [
7	30	93.8	226	2	C70790	probable Endonucle
8	30	93.8	237	2	GB8199	hypothetical prote
9	30	93.8	361	2	AG0169	phosphoserrine tran
10	30	93.8	362	2	C82372	hypothetical prote
11	30	93.8	403	2	T25524	hypothetical prote
12	30	93.8	415	2	T46716	probable myrosinase
13	30	93.8	465	2	A96553	tryptophan-tRNA I1
14	30	93.8	481	1	SS0053	monophenol monooxy
15	30	93.8	533	1	YRGCS	hypothetical prote
16	30	93.8	747	2	T16274	hypothetical prote
17	30	93.8	824	2	S40937	xeroderma pigmento
18	30	93.8	900	2	S70630	probable transport
19	30	93.8	940	2	S43345	AcB/ActD/ActF fam
20	30	93.8	1041	2	C87645	hypothetical prote
21	30	93.8	1564	2	S55517	ribosomal protein
22	27	84.4	36	2	H70351	hypothetical prote
23	27	84.4	60	1	F70187	hypothetical prote
24	27	84.4	199	2	T39498	hypothetical prote
25	27	84.4	201	2	A86636	purine-nucleoside
26	27	84.4	234	2	A84993	hypothetical prote
27	27	84.4	258	2	T22092	conserved hypothet
28	27	84.4	275	2	A69413	hypothetical prote
29	27	84.4	299	2	F64911	

add 5'-region hypo  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
endonuclease III -  
acetyl-CoA synthet  
uncharacterized co  
V-type sodium ATP  
Unknown protein en  
hypothetical prote  
YcfX protein - Esc  
probable enzyme [i  
probable EC 2.1 en  
probable ATP-bindi  
tryptophan-tRNA li  
peptidyl-prolyl ci

## ALIGNMENTS

RESULT 1  
B85684 unknown protein encoded by prophage CP-933C [Imported] - Escherichia coli (strain O157:H15)  
C;Species: Escherichia coli  
C;Date: 16-Feb-2001 #text\_change 14-Sep-2001  
C;Accession: B85684  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimambatta, Z.; Potamitis, K.; Apodaca,  
Nature 409, 529-533, 2001.  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85680; PMID:21074935; PMID:11206551  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-77 <STOP>  
A;Cross-references: GB:AE005174; NID:912514756; PIDN:AA955934.1; GSPDB:GN00145; UWGB:Z1.  
A;Experimental source: strain O157:H7, substrate EDL933  
A;Genetics:  
A;Gene: Z1836

RESULT 1  
B85684 Query Match 93.8%; Score 30; DB 2; Length 77;  
Best Local Similarity 100.0%; Pred. No. 9.8%; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0;

Qy	3 GFYRN 7
Db	15 GFYRN 19

RESULT 2  
S76180 Query Match 93.8%; Score 30; DB 2; Length 77;  
Best Local Similarity 100.0%; Pred. No. 9.8%; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0;

C;Variety: PCC 6803  
C;Date: 25-Apr-1997 #text\_change 08-Oct-1999  
C;Accession: S76180  
R;Kansko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O. K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-116, 1996  
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis  
s. A;Reference number: S74322; PMID:97061201; PMID:8905231  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-134 <KAN>  
A;Cross-references: EMBL:D90914; GB:AB001339; NID:9165477; PIDN:BA018439.1; PMID:di01917  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 93.8%; Score 30; DB 2; Length 134;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

Qy 3 GFYRN 7  
|||  
Db 27 GFYRN 31

## RESULT 3

BB7703 Conserved hypothetical protein CC3660 [imported] - Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001

C;Accession: BB7703

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolon

n, J.; Ermoljeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: AB7249; MUID:21173698; PMID:11259647

A;Accession: B87703

A;Molecule type: DNA

A;Residues: 1-172 &lt;STO&gt;

A;Cross-references: GB:AE005673; NID:913425418; PIDN:AAK25622.1; GSPDB:GN00148

C;Genetics: A;Gene: CC3660

Query Match 93.8%; Score 30; DB 2; Length 172;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 3 GFYRN 7  
|||  
Db 73 GFYRN 77

## RESULT 4

S73496 Hypoxanthine-guanine phosphoribosyltransferase hpt - Mycoplasma pneumoniae (strain ATCC

R;Hummelreich, R.; Hilpert, H.; Plagans, H.; Pirkle, E.; Li, B.C.; Herrmann, R.

R;Nucleic Acids Res. 24, 4420-4449, 1996

A;Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae

A;Reference number: S73327; MUID:97105885; PMID:8948633

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-175 &lt;HIM&gt;

A;Cross-references: EMBL:AE000018; GB:U00089; NID:91673827; PIDN:AB995818.1; PID:9167383

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C;Genetics: A;Gene: hpt

A;Genetic code: SGCG3

C;Superfamily: hypoxanthine phosphoribosyltransferase

Query Match 93.8%; Score 30; DB 2; Length 175;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 3 GFYRN 7  
|||  
Db 159 GFYRN 163

## RESULT 5

F64250 Hypoxanthine-guanine phosphoribosyltransferase - Mycoplasma genitalium

C;Species: Mycoplasma genitalium

C;Date: 17-Nov-1995 #sequence\_revision 17-Nov-1995 #text\_change 07-Dec-1995

C;Accession: F64250

A;Accession number: A05000; MUID:98295987; PMID:634320

A;Reference number: C70790

A;Molecule type: DNA

A;Status: preliminary

A;Cross-references: GB:U00089; NID:91673827; PIDN:AB995818.1; PID:9167383

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996

C;Genetics: A;Gene: hpt

A;Genetic code: SGCG3

C;Superfamily: hypoxanthine phosphoribosyltransferase

Query Match 93.8%; Score 30; DB 2; Length 175;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 3 GFYRN 7  
|||  
Db 89 GFYRN 93

## RESULT 6

AC2302 endonuclease III [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Dec-2002

C;Accession: AC2302

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamata, M.; Tabata, S.

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena sp. strain PCC 7120

A;Reference number: AB1807; MUID:21195285; PMID:11759340

A;Accession: AC2302

A;Molecule type: DNA

A;Status: preliminary

A;Cross-references: GB:BA000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

C;Superfamily: apurinic/aprimidinic endonuclease III

A;Accession: 1-1223 &lt;KUR&gt;

A;Cross-references: GB:U000019; PIDN:BA875669.1; PID:917133104; GSPDB:GN00179

A;Experiment source: strain PCC 7120

C;Genetics: A;Gene: nth

A;Cross-references: GB:AU022121; GB:AL123456; NID:93261559; PID:CAA17996\_1; PID:9296009  
 A;Experimental source: strain H37RV  
 C;Gene: nth  
 C;Superfamily: apurinic/aprimidinic endonuclease III  
 C;Keywords: 4Fe-4S; iron-sulfur Protein; metalloprotein  
 F:179,186-189,195/Binding site: 4Fe-4S cluster (cyt) (covalent) #status predicted

Query Match	93.8%;	Score 30;	DB 2;	Length 226;
Best Local Similarity	100.0%;	Pred. No.	29;	
Matches	5;	Conservative	0;	Mismatches 0;
Qy	3 GFYRN 7			
Db	72 GFYRN 76			

RESULT 8  
 Q84229  
 hypothetical protein Vng1457c [Imported] - Halobacterium sp. NRC-1  
 C;Species: Halobacterium sp. NRC-1  
 C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 C;Accession: GB4299  
 R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.; Leithauser, B.; Kehler, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabilic, P.; Jung, K.H.; Alam, M.; Freitas, T.  
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000  
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omar, A.D.; Ebbhardt, H.; Lowe, T.M.; Li A;Title: Genome sequence of Halobacterium species NRC-1.  
 A;Reference number: A84160; PMID:20504483; PMID:11016950  
 A;Accession: GB4299  
 A;Status: Preliminary  
 A;Residues: 1-237 <STO>  
 A;Molecule type: DNA  
 A;Cross-references: GB:AE004437; NID:910580953; PIDN:AGI19763\_1; GSPDB:GN00138  
 C;Genetics:  
 A;Gene: VNG1457C

Query Match 93.8%; Score 30; DB 2; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	3 GFYRN 7			
Db	191 GFYRN 195			

RESULT 9  
 AG0169

phosphoserine transamidase (EC 2.6.1.52) [Imported] - Yersinia pestis (strain C092)  
 C;Species: Yersinia pestis  
 C;Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 27-Nov-2001  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; IJ, M.; Rutledge, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Davidson, S.; Wohldmann, P.; Subramanian, S.; Quail, M.A.; Churcher, C.; Mungall, K.; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; IJ, M.; Rutledge, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, B.; Nature 413, 523-527, 2001  
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A;Reference number: AB0001; PMID:21470413; PMID:115636360  
 A;Accession: AG0169  
 A;Status: preliminary  
 A;Residues: 1-361 <KUR>  
 A;Cross-references: GB:AL590842; PIDN:CACS0218\_1; PID:915979438; GSPDB:GN00175  
 C;Genetics:  
 C;Superfamily: phosphoserine aminotransferase

Query Match 93.8%; Score 30; DB 2; Length 361;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C;Species: serC

C;Superfamily: phosphoserine aminotransferase

C;Genetics: serC

C;Superfamily: aminotransferase

C;Genetics: aminotransferase

C;Superfamily: aminotransferase

C;Genetics: aminotransferase

C;Superfamily: aminotransferase

C;Genetics: aminotransferase

A;Cross-references: PID:9296009  
 A;Experimental source: strain H37RV  
 C;Gene: nth  
 C;Superfamily: apurinic/aprimidinic endonuclease III  
 C;Keywords: 4Fe-4S; iron-sulfur Protein; metalloprotein  
 F:179,186-189,195/Binding site: 4Fe-4S cluster (cyt) (covalent) #status predicted

Query Match	93.8%;	Score 30;	DB 2;	Length 226;
Best Local Similarity	100.0%;	Pred. No.	29;	
Matches	5;	Conservative	0;	Mismatches 0;
Qy	3 GFYRN 7			
Db	72 GFYRN 76			

RESULT 10  
 C82572  
 phosphoserine aminotransferase XF2326 [imported] - Xylella fastidiosa (strain 95c)  
 C;Species: Xylella fastidiosa  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Sep-2000  
 C;Accession: C82572  
 R;Anonymous: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
 Nature 406, 151-157, 2000  
 A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
 A;Reference number: A82515; PMID:1065717; PMID:10910347  
 A;Note: for a complete list of authors see reference number A59328 below  
 A;Accession: C82572  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-362 <SIM>  
 C;Cross-references: GB:AE004043; GB:AE003849; PIDN:AAFF85125\_1; GSPDB:GN001

A;Experimental source: strain 95c  
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Aencio, M.; Alvarenga, R.; A  
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.E.A.; Carrato, D.M.; Carrer, H.;  
 da Neto, E.; Docena, C.; El-Dorry, H.; Ferreira, A.P.; Ferreira, A.J.S.  
 Submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, M.C.; Frohm  
 J.D.; Junqueira, M.L.; Kember, E.L.; Kitajima, J.B.; Krieger, J.P.; Kurama, H.M.F.; Marins, E.; Martins, B.C.M.; Miracqua, C.Y.; Miyaki, C.Y.; Rodrigues, V.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmeiro, M.C.; de Oliveira, R.C.; Santelli, R.V.; Sawasaki, M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Contents: annotations  
 C;Genetics:  
 A;Gene: XF326  
 C;Superfamily: phosphoserine aminotransferase

Query Match 93.8%; Score 30; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 47;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7

Db 284 GFYRN 288

RESULT 11  
 T25524  
 hypothetical protein C06A5\_9 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T25524  
 R;Davidson, S.; Wohldmann, P.; submitted to the EMBL Data Library, April 1997

A;Description: The sequence of C. elegans cosmid C06A5 .

A;Reference number: 220044  
 A;Accession: T25524  
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA  
 A;Residues: 1-408 <DAV>

A;Cross-references: EMBL:U97193; PIDN:AB52442\_1; GSPDB:GN00019; CESP:CO6A5\_9

A;Experimental source: strain Bristol N2; clone C06A5

C;Genetics:  
 A;Gene: CESP:CO6A5\_9

A;Map Position: 1  
 A;Introns: 3/1; 27/3; 86/1; 154/1; 201/3; 240/3; 268/3; 297/3

Query Match 93.8%; Score 30; DB 2; Length 408;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

C;Genetics:  
 A;Gene: CESP:CO6A5\_9

RESULT 12

Qy 3 GFYRN 7  
Db 229 GFYRN 233

Hypothesetical protein L4326\_05 [imported] - Leishmania major

C;Species: Leishmania major  
C;Date: 18-Feb-2000 #sequence\_revision 18-Feb-2000 #text\_change 18-Feb-2000  
C;Accession: T46716  
R;Volckaert, G.; Ivens, A.C.; Lawson, D.; Quail, M.; Rajandream, M.A.; Barrell, B.G.  
Submitted to the EMBL Data Library, December 1999  
A;Reference number: 223137  
A;Accession: T46716  
A;Status: preliminary; translated from GB/EMBL/DDJB  
A;Molecule type: DNA  
A;Residues: 1-415 <VOL>  
A;Cross-references: EMBL:Ali21861; PIDN:CAA858381.1  
A;Experimental source: strain Friedlin  
C;Genetics:  
A;Note: L4326\_05

Query Match 93.8%; Score 30; DB 2; Length 415;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7  
Db 325 GFYRN 329

RESULT 13

A96553 probable tyrosinase precursor 53323\_50499 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Accession: A96553  
RTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Hughes, M.K.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.J.; Huizer, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.R.; Li, Y.; Lin, X.; Liu, S.X.; Liu, T.; Luos, J.S.; Maiti, R.; Marzali, C.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the Plant Arabidopsis.  
A;Reference number: A86141; PMID:21016719; PMID:11130712  
A;Accession: A96553  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-465 <STO>  
C;Genetics:  
A;Gene: F5D21\_17  
C;Superfamily: Agrobacterium beta-glucosidase

Query Match 93.8%; Score 30; DB 2; Length 465;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7  
Db 331 GFYRN 335

RESULT 14

SS0053 tryptophan-tRNA ligase (EC 6.1.1.2) alpha-2 chain - mouse  
C;Species: Mus musculus (house mouse)

R/Terao, M.; Tabe, L.; Garattini, E.; Sartori, D.; Studer, M.; Mintz, B.  
 A/Biochem.: Isolation and characterization of variant cDNAs encoding mouse tyrosinase.  
 A/Reference number: A32499  
 A/Molecule type: mRNA  
 A/Cross-references: GB:M24560; NID:920249; PMID:9202250  
 A/Accession: B3429

A/Molecule type: mRNA  
 A/Residues 1-77:155-345,'G',347-533 <TE2>

A/Cross-references: GB:M24560

A/Experimental source: B16 melanoma cells

R/Mueiller, G.; Ruppert, S.; Schmid, E.; Schuetz, G.

EMBO J. 7, 2723-2730, 1988

A/Title: Functional analysis of alternatively spliced tyrosinase gene transcripts.

A/Reference number: S01170; MUID:89030636; PMID:3141148

A/Molecule type: mRNA  
 A/Residues 1-102,'C',104-263,'I',265-345,'G',347-533 <MCB>

A/Cross-references: GB:XI12782; NID:955161; PIDN:CAA1273-1; PMID:955062

R/Yamamoto, H.; Takeuchi, S.; Kudo, T.; Makino, K.; Nakata, A.; Shinoda, T.; Takeuchi, T.

Proc. J. Genet. 62, 271-274, 1987

A/Title: Cloning and sequencing of mouse tyrosinase cDNA.

A/Reference number: S02278

A/Molecule type: mRNA  
 A/Residues 1-102,'C',104-263,'I',265-345,'G',347-448 <YAM>

A/Cross-references: EMBL:XI12782

A/Note: part of this sequence was confirmed by protein sequencing

R/Shibahara, S.; Okinaga, S.; Tomita, Y.; Takeda, A.; Yamamoto, H.; Sato, M.; Takeuchi,

Proc. J. Biochem. 189, 455-461, 1990

A/Title: A point mutation in the tyrosinase gene of BALB/c albino mouse causing the cysteine

A/Reference number: S15753; MUID:90249393; PMID:2110899

A/Status: translation not shown

A/Molecule type: DNA  
 A/Residues 1-13 <SH>

A/Cross-references: EMBL:X51743; NID:955057; PIDN:CAA36033.1; PMID:955058

A/Experimental source: strain BALB/c

R/Kwon, B. S.; Halabon, R.; Chintamaneni, C.

Biochem. Biophys. Res. Commun. 167, 251-260, 1989

A/Title: Molecular basis of mouse Himalayan mutation.

A/Reference number: I49736; MUID:99273644; PMID:2567165

A/Accession: I49736

A/Molecule type: Preliminary; translated from GB/ENBL/DBJ

A/Residues 1-39,'I',41-102,'C',104-196,'Q',198-345,'G',347-419,'R',421-533 <REB>

A/Cross-references: GB:M26729; NID:919345; PIDN:AA37806.1; PMID:9309296

C/Comment: This cell-specific oxidase is a glycoprotein containing two Cu per enzyme; it reacts in the formation of pigments such as melanins and other polyphenolic compound C/Genetics:

A/Gene: TYR1

A/Map Position: 7

C/Superfamily: monophenol monooxygenase

C/Keywords: albinism; alternative splicing; copper; glycoprotein; melanin biosynthesis;

C/Keywords: F1-18-Domain; signal sequence #status Predicted <SG>

F19-533/Product: monophenol monooxygenase #status Predicted <TM>

F1474-497/Domain: Transmembrane #status Predicted <TM>  
 F:86,111,161,230,337,371/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 93.8%; Score 30; DB 1; Length 533;

Best Local Similarity 100.0%; Pred. No. 69; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7

Db 458 GFYRN 462



BIOSEARCH RESULTS									
SEARCHED: 141681 seqs., 52070155 residues									
SEARCHED: 141681 seqs., 52070155 residues									
SEARCHED: 141681 seqs., 52070155 residues									
SEARCHED: 141681 seqs., 52070155 residues									
Total number of hits satisfying chosen parameters:									
Minimum DB seq length: 0									
Maximum DB seq length: 2000000000									
Post-processing: Minimum Match 0%									
Maximum Match 100%									
Listing first 45 summaries									
Database : SwissProt 42.1									
Predicted No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
Result No.	Score		Query Match Length		DB ID		Description		
1	30		93.8		175		P41696 mycoplasma P75119 mycoplasma		
2	30		93.8		175		P63642 mycoplasma		
3	30		93.8		245		P43303 microccoccus		
4	30		93.8		279		P1UVN_MICLUT		
5	30		93.8		361		SERC_XANAC		
6	30		93.8		361		SERC_XANCP		
7	30		93.8		361		SERC_YERPE		
8	30		93.8		362		SERC_XYLPA		
9	30		93.8		362		SERC_XYLFI		
10	30		93.8		378		SERC_RALSO		
11	30		93.8		423		PUR2_RHIME		
12	30		93.8		481		SYW_WOUSE		
13	30		93.8		533		TYRO_MOUSE		
14	30		93.8		824		YOT5_CAEEL		
15	30		93.8		900		XPC_MOUSE		
16	30		93.8		939		YF35_METJU		
17	30		93.8		1564		PDR4 YEAST		
18	27		84.4		59		RL32_BORBU		
19	27		84.4		201		YAUF_LACLA		
20	27		84.4		218		KAD_CHLTE		
21	27		84.4		234		DEOB_BUCAI		
22	27		84.4		299		YF35_METJU		
23	27		84.4		318		SOLR_CLOAB		
24	27		84.4		320		K6PF_BUCAF		
25	27		84.4		340		YD17_ARCFU		
26	27		84.4		344		Y613_METJU		
27	27		84.4		465		YCXJ_ECOLI		
28	27		84.4		471		SYW_HUMAN		
29	27		84.4		471		YAL5_SCHEPO		
30	27		84.4		475		SYW_BOVIN		
31	27		84.4		475		SYW_RABIT		
32	27		84.4		492		ANKH_RAT		
33	27		84.4		492		P25864_arabidopsis		
34	27		84.4		506		CSLB_PEDBACTER		
35	27		84.4		530		Q96CW9_homo_sapien		
36	27		84.4		550		P12944_desulfobiv		
37	27		84.4		589		Q8r4f1_mus_musculus		
38	27		84.4		608		Q8zwk4_pyrococcum		
39	27		84.4		667		Q03185_giardia_lam		
40	27		84.4		713		P21849_giardia_lam		
41	26		81.2		91		V179_FOWPV		
42	26		81.2		179		Q8ct97_staphylococ		
43	26		81.2		194		P11894_pisum_sativ		
44	26		81.2		197		RK9_FEARATH		
45	26		81.2		218		YAF5_LACLA		

DR TIGR; MG458; -; Hxn\_phospho\_trans.  
 DR InterPro; IPR005904; Hxn\_phospho\_trans.  
 DR InterPro; IPR002375; Pr/PY\_RP\_transf.  
 DR InterPro; IPR000336; PR/Py\_RP\_transf.  
 DR Pfam; PF00156; Ribosyltran; 1.  
 DR TIGRFAMS; TIGR01203; HGPRtase; 1.  
 DR PROSITE; PS00103; PUR\_Pyr\_PR\_TRANSFER; 1.  
 DR Transferase; GlycosylTransferase; Purine salvage; Metal-binding;  
 KW Magnesium; Complete proteome;  
 KW Magnesium; Complete proteome;  
 FT METAL -156 ; MAGNESIUM 1 (BY SIMILARITY).  
 SQ SEQUENCE 175 AA; 156 MAGNESIUM 1 (BY SIMILARITY).  
 FT METAL 19620 MW; 1E5A9AA01D69884 CRC64;  
 SQ  
 Query Match 93.8%; Score 30; DB 1; Length 175;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 5; Conservative 0; Mismatches 0; Gaps 0;  
 Indels 0;  
 Qy 3 GFYRN 7  
 Db 159 GFYRN 163  
 RESULT 3  
 END3 MYCTU\_NYCTU STANDARD; PRT; 245 AA.  
 ID END3\_NYCTU AC  
 AC 061642; DT 30-MAY-2000 (Rel. 39, Created)  
 OC 061642; DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Endonuclease III (EC 4.2.39.18) (DNA-(apurinic or apyrimidinic site)  
 DE lyase).  
 DE NIH OR RV3674C OR MT3775 OR MTW025 .022C OR MB3698C.  
 OS Mycobacterium tuberculosis, and  
 OS Mycobacterium bovis.  
 BC Actinobacteria; Actinomycetales;  
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 NCBI\_TaxID=1773; 1765;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX SPECIES=M.tuberculosis; STRAIN=H37rv;  
 RA MEDLINE=98295987; PubMed=0634230;  
 RA Cole S.T., Brosch R., Partchill J., Garnier T., Churcher C., Harris D.,  
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Telzai F., Connor R.,  
 RA Badcock K., Basham D., Brown D., Chillingworth T., Holroyd S.,  
 RA Davies R., Devlin K., Peilwell T., Gentles S., Haalin N., Holroyd S.,  
 RA Hornsby T., Jagels K., Kirgh A., McLean J., Moule S., Murphy L.,  
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 RA Rutter S., Seeger K., Skelton S., Squars S.,  
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RT "Deciphering the biology of Mycobacterium tuberculosis from the  
 complete genome sequence,"  
 RT laboratory strains.",  
 RL Nature 393:537-544 (1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;  
 RA MEDLINE=2221036; PubMed=0634230;  
 RX Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 RA Petersen J., Desoy R., Dodson R., Gwinn M., Haft D., Hickey E.,  
 RA Kolonay J.F., Nelson W.C., Omayam L.A., Ermolaeva M., Salzberg S.L.,  
 RA Delcher A., Utterback T., Weidman J., Gordon S.V., Wheeler P.R.,  
 RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.,  
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and  
 laboratory strains,"  
 RL J. Bacteriol. 184:5479-5490 (2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX SPECIES=M.bovis; STRAIN=AF2122/97;  
 RA MEDLINE=2270910; PubMed=12788972;  
 RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,  
 RA Pryor M., Dutchoy S., Grondin S., Lacroix C., Monsempé C., Simon S.,  
 RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,  
 RT "The complete genome sequence of Mycobacterium bovis,"  
 RT Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).  
 RL CC -!- FUNCTION: Has both an apurinic and/or apyrimidinic endonuclease  
 CC activity and a DNA N-glycosylase activity. Incises damaged DNA at  
 CC cytosines, thymines and guanines. Acts on a damaged strand, 5'  
 CC from the damaged site. (By similarity).  
 CC -!- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or  
 CC apyrimidinic site in DNA is broken by a beta-elimination reaction,  
 CC leaving a 3'-terminal unsaturated sugar and a product with a  
 CC terminal 5'-phosphate.  
 CC -!- COFACTOR: Binds a 4Fe-4S cluster which is not important for the

catalytic activity, but which is probably involved in the proper positioning of the enzyme along the DNA strand (By similarity).  
!- SIMILARITY: Belongs to the nth/muty family.

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DR EMBL; AL022121; CAA17996\_1; ALT\_INIT.  
DR EMBL; AE007175; AA48142\_1; ALT\_INIT.  
DR EMBL; BX28346; CAD95884\_1; .  
DR HSSP; P20625; 2ABK.  
DR TIGR; MT3715; .  
DR Tuberculist; Rv3674c; .  
DR InterPro; IPR03265; Endo\_3c.  
DR InterPro; IPR00435; Endo\_I\_FCL.  
DR InterPro; IPR00436; Endo\_II\_HhH.  
DR InterPro; IPR033651; FeS\_bind.  
DR InterPro; IPR00445; HhH.  
DR InterPro; IPR003583; Hhh\_1.  
DR InterPro; IPR005759; Nth.  
DR Pfam; PF00730; HhH\_GPD; 1.  
DR Pfam; PF00633; HHH; 1.  
DR SMART; SMO00478; END03c; 1.  
DR SMART; SMO00525; RES; 1.  
DR SMART; SMO0278; HHH1; 1.  
DR TIGRFAMS; TIGR01083; nth; 1.  
DR PROSITE; PS00754; ENDONUCLEASE\_III\_1; 1.  
DR PROSITE; PS01155; ENDONUCLEASE\_III\_2; 1.  
DR Hydrolase; Nuclease; Endonuclease; Multifunctional enzyme; DNA repair;  
KW Glycosidase; lyase; Iron-sulfur; 4Fe-4S; Complete proteome.  
PT METAL 198 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).  
PT METAL 205 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).  
PT METAL 208 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).  
PT METAL 214 IRON-SULFUR (4Fe-4S) (BY SIMILARITY).  
SQ SEQUENCE 245 AA; 2B6D16195DD090DE CRC64;

Query Match Score 93.8%; Score 30; DB 1; Length 245;  
Best Local Similarity 100.0%; Pred. No. 19,  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 3 GFYRN 7  
Db 91 GFYRN 95

RESULT 4  
UVEN\_MICLU STANDARD; PRT; 279 AA.

ID UVEN\_MICLU  
AC P46303  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ultraviolet N-glycosidase/NP lyase (UV-endonuclease) (Pyrimidine dimer glycosidase).  
DE Glycosidase.  
GN Micrococcus luteus (Micrococcus lysodeikticus).  
OC Bacteria; Actinobacteria; Actinomycetales;  
OC Micrococcineae; Micrococcaceae; Micrococcus.  
OX NCBI\_TaxID=1270;  
RN [1] SEQUENCE FROM N.A. AND SEQUENCE OF 1-35.

RC STRAIN=ATCC 4698;  
RX MEDLINE=96007490; Pubmed=7559510;  
RA Piersen C.E., Prince M.A., Augustine M.L., Dodson M.L., Lloyd R.S.;  
RT "Purification and cloning of Micrococcus luteus ultraviolet  
endonuclease, an N-glycosidase/abasic lyase that proceeds via an  
imino enzyme DNA intermediate," J. Biol. Chem. 270:23475-23484 (1995);  
RA Quaggio R.B., Monteiro-Vitorelo C.B., Van Sluys M.A., Ameida N.F.,  
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

CC -!- FUNCTION: Has both, an apurinic and/or pyrimidinic endonuclease activity and a DNA N-glycosidase activity. Initiates repair at CC cis-syn pyrimidine dimers. Proceeds via an imino enzyme:DNA intermediate.  
CC -!- MISCELLANEOUS: Readthrough of the terminator UAG occurs between codons for GLY-268 and Ala-270. Two forms of 31 kDa and 32 kDa have been detected.  
CC -!- SIMILARITY: Belongs to the nth/muty family.  
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CC or EMBL; U22181; AA86508\_1; ALT\_TERM.  
DR HSSP; P20625; 2ABK.  
DR InterPro; IPR003265; Endo\_3c.  
DR InterPro; IPR00435; Endo\_I\_FCL.  
DR InterPro; IPR00436; Endo\_II\_HhH.  
DR InterPro; IPR033651; FeS\_bind.  
DR InterPro; IPR00445; HhH.  
DR InterPro; IPR003583; Hhh\_1.  
DR InterPro; IPR005759; Nth.  
DR PROSITE; PS00754; ENDONUCLEASE\_III\_1; 1.  
DR PROSITE; PS01155; ENDONUCLEASE\_III\_2; 1.  
DR Hydrolase; Nuclease; Endonuclease; DNA repair; Glycosidase;  
KW Iron-sulfur; Endonuclease; DNA repair; Glycosidase;  
KW UV ENDONUCLEASE 31 kDa FORM.  
KW UV ENDONUCLEASE 32 kDa FORM (PROBABLE).  
FT CHAIN 1 268  
FT CHAIN 1 279  
FT METAL 203  
FT METAL 210  
FT METAL 213  
FT METAL 219  
SQ SEQUENCE 279 AA; C38536A187C005 CRC64;  
Query Match Score 93.8%; Score 30; DB 1; Length 279;  
Best Local Similarity 100.0%; Prtd. No. 22;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7  
Db 95 GFYRN 99

RESULT 5  
SERC\_XANAC STANDARD; PRT; 361 AA.  
ID SERC\_XANAC  
ID QBPFL7;  
AC DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DB Phosphoserine aminotransferase (EC 2.6.1.52) (PSAT).  
GN SERC OR XAC168.  
OS Xanthomonas axonopodis (pv. citri).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;  
OC Xanthomonadaceae; Xanthomonas.  
OX NCBI\_TaxID=92029;  
RN [1] SEQUENCE FROM N.A.  
RP STRAIN=306 / ATCC 13902 / XV 101;  
RC MEDLINE=2202245; Pubmed=12024217;  
RX da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,  
RA Quaggio R.B., Monteiro-Vitorelo C.B., Van Sluys M.A., Ameida N.F.,  
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,  
 RA Ciccarelli R.M.B., Cordeiro L.L., Cursino-Santos J.R., El-Dorzy H.,  
 RA Faia J.B., Ferreira A.J.S., Ferreira R.C.C., Perio M.I.T.,  
 RA Formighieri B.F., Franco M.C., Greggio C.C., Gruber A.,  
 RA Katsuyama A.M., Kishi L.T., Lete R.P., Lemos E.G.M., Lemos M.V.F.,  
 RA Locali E.C., Machado M.A., Madreia A.M.B.N., Martine Rossi N.M.,  
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,  
 RA Moreira T.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,  
 RA Pereira H.A., Rossi A., Souza R.F., Teixeira E.C., Tezza R.I.D.,  
 RA Spinola L.A.P., Tikitka M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,  
 RA Terubaud dos Santos M., Tsai S.M., White F.P.,  
 RA Setubal J.C., Kitajima J.P.,  
 RA "Comparison of the genomes of two Xanthomonas pathogens with differing  
 host specificities." ;  
 RIRL Nature 417:459-463 (2002).  
 RIRL CATALYTIC ACTIVITY: O-phospho-L-serine + 2-oxoglutarate = 3-  
 RIRL phosphonoxypropanoate + L-glutamate.  
 RIRL COFACTOR: Pyridoxal phosphate (By similarity).  
 RIRL PATHWAY: Required both in major phosphorylated pathway of serine  
 RIRL biosynthesis and in the biosynthesis of pyridoxine (By  
 RIRL similarity).  
 RIRL SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 RIRL SIMILARITY: Belongs to Class-V of pyridoxal-phosphate-dependent  
 RIRL aminotransferases.  
 RIRL

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Query Match 93.8%; Score 30; DB 1; Length 361;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 5; Conservative 0%; Mismatches 0%; Indels

3 GFYRN 7  
| | | |

b 283 GFYRN 287

Qry	3 GFYRN 7	3 GFYRN 287	Best Local Similarity 100.0% ; Matches 5;	Length 282 ; Pred. No. 28 ; Mismatches 0 ; Conservative 0 ; Indels 0 ; Gaps 0 ;	Length 282 ; Pred. No. 28 ; Mismatches 0 ; Conservative 0 ; Indels 0 ; Gaps 0 ;
<b>RESULT 7</b>					
SERC_YERPE	SERC_YERPE	STANDARD;	PRT;	361 AA.	
ID	Q8ZG84;				
AC					
DT	10-OCT-2003	(Rel. 42, Created)			
DT	10-OCT-2003	(Rel. 42, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DEF		Phosphoserine aminotransferase (EC 2.6.1.52)	(PSAT).		
GN	SERC OR YFO1389 OR Y2784.				
OS	Yersinia pestis.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; Yersinia.				
OX	NCBI_TaxID=632;				
[1]					
SEQUENCE FROM N.A.					
RC	RP				
RC	SEQUENCE=CO-92 / Biivar Orientalis;				

MEDLINE=21470413; PubMed=11586360;  
 RX Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
 RA Prentice M.B., Sebaiinia M., James K.D., Churcher C., Mungall K.L.,  
 RA Baker S., Basham D., Bentle S.D., Brooks P., Cerdeno-Taronga A.M.,  
 RA Chillingworth T., Cronin A., Davies R.M., Dougan G.,  
 RA Feltwell T., Hamlin N., Holroyd S., Jageis K., Karlyshev A.V.,  
 RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,  
 RA Simmonds M., Skeleton J., Stevens K., Whitehead S., Barrell B.G.,  
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague.";  
 RL Nature 413:523-527(2001).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN-KIMS / Bicovar Mediolavalis;  
 MEDLINE=22137863; PubMed=12142430;  
 RX Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,  
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,  
 RA Fetherston J.D., Lindler L.B., Brubaker R.R., Plano G.V., Blattner F.R.,  
 RA Straley S.C., McWhorter K.A., Nilles M.L., Matson J.S., Blattner F.R.,  
 RT Perry R.D.;  
 RT "Genome sequence of *Yersinia pestis* KIM.";  
 RL Bacillus 184:4601-4611(2002).  
 CC -|- CATALYTIC ACTIVITY: O-phospho-L-serine + 2-oxoglutarate = 3-  
 phosphonoxypropruvate + L-glutamate.  
 CC -|- COFACTOR: Pyridoxal phosphate (By similarity).  
 CC -|- PATHWAY: Required both in major phosphorylated pathway of serine  
 biosynthesis and in the biosynthesis of pyridoxine (By  
 similarity).  
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -|- SIMILARITY: Belongs to class-V of pyridoxal-phosphate-dependent  
 aminotransferases.

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 or send an email to license@isb-sib.ch).

CC -|- DR EMBL; AU414148; CAC09218.1; -.

DR PIR; AE013881; AMB86336.1; -.

DR HAMAP; MF\_00169; AG0169.

DR InterPro; IPR000192; Aminotrans V.

DR InterPro; IPR000248; Pser amintransf.

DR Pfam; PF00266; aminotran\_5; 1.

DR Prod0m; PD001544; Pser\_amintransf; 1.

DR TIGRFAMs; TIGR01364; serC1; 1.

DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; 1.

DR Serine biosynthesis; Pyridoxine biosynthesis; Transferase;

KW Aminotransferase; Pyridoxal phosphate; Complete proteome;

FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).

SQ SEQUENCE 361 AA; 40083 MW; 88278F1419782D88 CRC64;

Query Match 93.8%; Score 30; DB 1; Length 361;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy

3 GFYRN 7  
 |||||  
 Db 283 GFYRN 287

RESULT 8  
 SERC\_XYLFA STANDARD; PRT; 362 AA.  
 ID SERC\_XYLFA  
 AC Q9P19; DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DB Phosphoserine aminotransferase (EC 2.6.1.52) (PSAT).  
 GN SERC OR XP326.  
 OX Xylella fastidiosa.

SEQUENCE FROM N.A.  
 OC Xanthomonadaceae; Xylella.  
 OC NCBI\_TaxID=2311;  
 RN RP  
 RC STRAIN=95C;  
 RX MEDLINE=20365117; PubMed=10910347;  
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acedio M.,  
 RA Alvarezga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,  
 RA Barrios M.H., Bonacorsi E.D., Bordin S., Bove J.M., Brito M.R.S.,  
 RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carrasco D.M., Carrer H.,  
 RA Colauto N.B., Colombo C., Costa M.C.R., Costa-Neto C.M.,  
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,  
 RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,  
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,  
 RA Garner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,  
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper B.L., Kitajima J.P.,  
 RA Krieger J.E., Kuramae E.E., Laigre D., Lambais M.R., Leite L.C.C.,  
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,  
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Martins E.M.F.,  
 RA Marques M.V., Martins B.A.L., Martins E.C.C., Miyazaki C.Y., Monteiro-Vitorello C.B.,  
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,  
 RA Nhami A.Jr., Nobrega G., Nunes L.R., Oliveira M.A.,  
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,  
 RA Peixoto B.R., Pereira G.A.G., Pereira H.A.J., Pesquero J.B.,  
 RA Quaggio R., Roberto P.G., Rodrigues V., de Ross A.J.M.,  
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,  
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,  
 RA da Silveira J.F., Silveira M.L.Z., Siqueira W.J., de Souza A.A.,  
 RA de Souza A.P., Teranzi M.F., Truffi D., Tsai S.M., Tsuahiko M.H.,  
 RA Valada H., Van Siuys M.A., Verjovski-Almeida S., Vettore A.L.,  
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;  
 RT "The genome sequence of a plant pathogen *Xylella fastidiosa*.";  
 CC -|- CATALYTIC ACTIVITY: O-phospho-L-serine + 2-oxoglutarate = 3-  
 phosphonocypyruvate + L-glutamate (By similarity).  
 CC -|- COFACTOR: Pyridoxal phosphate (By similarity).  
 CC -|- PATHWAY: Required both in major phosphorylated pathway of serine  
 biosynthesis and in the biosynthesis of Pyridoxine (By  
 similarity).  
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -|- SIMILARITY: Belongs to Class-V of pyridoxal-phosphate-dependent  
 aminotransferases.

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 or send an email to license@isb-sib.ch).  
 CC -|- DR PIR; AB004047; AA85125.1; -.

DR PIR2572; CB2572.  
 DR HSSP; P23721; 1BJN.  
 DR HAMP; MF\_00160; -; 1.  
 DR InterPro; IPR000192; Aminotrans V.  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR Prod0m; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; serC1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 SQ SEQUENCE 362 AA; 39615 MW; E0CE351A7A6276A4 CRC64;

DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR Prod0m; PD001544; Pser amintransf; 1.  
 DR HSSP; P23721; 1BJN.  
 DR HAMP; MF\_00160; -; 1.  
 DR InterPro; IPR000192; Aminotrans V.  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
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 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
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 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
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 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
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 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
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 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5; 1.  
 DR PRODOM; PD001544; Pser amintransf; 1.  
 DR TIGRFAMs; TIGR01364; SERC\_1; 1.  
 DR PROSITE; PS00595; AA\_TRANSFER\_CLASS\_5; FALSE NEG.  
 KW Serine biosynthesis; Pyridoxine biosynthesis; Transferase;  
 KW Aminotransferase; Pyridoxal phosphate; Complete proteome.  
 FT BINDING 197 197 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
 DR PFam; PF00266; aminotran\_5;



DE Phosphoribosylamine-glycine ligase (EC 6.3.4.13) (GARS) (Glycynamide ribonucleotide synthetase) (Phosphoribosylglycynamide synthetase).  
 DB RIBONUCLEOTIDE SYNTHETASE  
 RN 11; NCBI\_TaxID=382;  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=1021;  
 RX MEDLINE=21396507; PubMed=11481430;  
 RA Capela D., Barloy-Rhubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
 RA Godrie T., Goiffau A., Kahn D., Kles E., Lejaire V., Masuy D.,  
 RA Pohl T., Porteille D., Puehler A., Purnelle B., Ramsperger U.,  
 RA Renard C., Thébaud P., Vandembrou M., Weidner S., Galibert F.;  
 RT Sinorhizobium meliloti strain 1021;"  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
 CC -!- CATALYTIC ACTIVITY: ATP + 5'-phospho-D-ribosylglycynamide + glycine = ADP  
 CC + Phosphate + N(1)-(5'-phospho-D-ribosyl)glycynamide.  
 CC -!- PATHWAY: De novo purine biosynthesis; second step.  
 CC -!- SIMILARITY: Belongs to the GARS family.

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CC EMBL; AL591785; CAC15430.1; -.  
 CC HAMAP; MF\_00138; -!- 1.  
 DR InterPro; IPR000115; Gars.  
 DR Pfam; PF01071; GARS\_1.  
 DR Pfam; PF02842; GARS\_B; 1.  
 DR Pfam; PF02843; GARS\_C; 1.  
 DR Pfam; PF02844; GARS\_N; 1.  
 DR TIGRFAMS; TIGR00877; purd\_1.  
 DR PROSITE; PS001384; GARS\_1.  
 KW Purine biosynthesis; Ligase; Complete proteome.  
 SQ SEQUENCE 423 AA; 44324 MW; SE65E13B06D204B CRC64;  
 Query Match 93.8%; Score 30; DB 1; Length 423;  
 Best Local Similarity 100.0%; Pred. No. 33;  
 Matches 5; Conservative 0; Mismatches 0; Gaps 0;  
 Qy 3 GPYRN 7  
 Db 407 GFYRN 411

RESULT 12  
 SYW\_MOUSE  
 ID SYW\_MOUSE STANDARD PRT; 481 AA.  
 AC P32921;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase) (TRPS).  
 DB WARS OR WRS.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Nematoda; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1] SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RX MEDLINE=95018226; PubMed=1932716;  
 RA Pajot B., Sarger C., Bonnet J., Garret M.;  
 RT An alternative splicing modifies the C-terminal end of tryptophanyl-tRNA synthetase in murine embryonic stem cells.";

RL J. Mol. Biol. 242:599-603 (1994). CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA (Trp) = AMP + diphosphate + L-tryptophanyl-tRNA (Trp).  
 CC -!- SUBUNIT: Homodimer. (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1; Synonyms=Long;  
 CC IsoID=P32921-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Short;  
 CC IsoID=P32921-2; Sequence=VSP\_006312;  
 CC -!- TISSUE SPECIFICITY: Isoform 2 is widely expressed, isoform 1 is found only in embryonic stem cells.  
 CC -!- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.  
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 CC EMBL; X69656; CAA49347.1; -.  
 DR PRT; X69657; CAA49348.1; -.  
 DR PRT; S50053; S50053.  
 DR MGII; 104630; Wars.  
 DR InterPro; IPR002305; tRNA-synt\_1b.  
 DR InterPro; IPR01412; tRNA-synt\_I.  
 DR InterPro; IPR002306; Trp\_tRNA-synt\_1b.  
 DR InterPro; IPR000738; WHEP-TRS.  
 DR Pfam; PF00459; tRNA-synt\_1b; 1.  
 DR Pfam; PF0458; WHEP-TRS; -!- 1.  
 DR PRINTS; PR01039; TRNASTH-TRP.  
 DR TIGRFAMS; TIGR00233; TRDS; 1.  
 DR PROSITE; PS00178; AA\_TRNA\_LIGASE\_I; 1.  
 DR PROSITE; PS00762; WHEP-TRS; 1.  
 DR Pfam; PF00459; tRNA-synt\_1b; 1.  
 DR Alternative splicing. WHEP-TRS.  
 FT DOMAIN 23 68 "HIGH" REGION.  
 FT SITE 168 177 "KMSKS" REGION.  
 FT SITE 353 357 Missing (in isoform 2).  
 FT VARSPPLIC 476 481 /FTID=VSP\_006313.  
 SQ SEQUENCE 481 AA; 54282 MW; B05A452C08074F52 CRC64;  
 Query Match 93.8%; Score 30; DB 1; Length 481;  
 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GPYRN 7  
 Db 250 GFYRN 254

RESULT 13  
 TYRO\_MOUSE STANDARD PRT; 533 AA.  
 AC P11214;  
 AC 01-JUL-1989 (Rel. 11, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Tyrosinase precursor (EC 1.14.18.1) (Monoghenol monooxygenase) (Albinino locus protein).  
 GN TYR  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCB\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DBA/2J; PubMed=3134020;  
 RC MEDLINE=88268310; PubMed=3134020;



OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peioderinae; Caenorhabditis.  
 RN NCBI\_TAXID=6239;  
 [1] SEQUENCE FROM N.A.

STRAIN\_BRISTOL\_N2; PubMed=7906398;  
 RX MEDLINE=94150718; PubMed=7906398;  
 RA Wilson R., Ainscough R., Anderson K., Berks C., Baynes C., Berks M., Couplson A.,  
 RA Bonfield J., Burton J., Connell M., Coppey T., Cooper J., Coulson A.,  
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,  
 RA Fulton L., Gardner A., Green P., Hawkin T., Hillier L., Jier M.,  
 RA Johnson L., Jones M., Kershaw J., Kirsten J., Laisser N.,  
 RA Latrell P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,  
 RA Parsons J., Percy C., Riiken L., Roopra A., Saunders D., Showman R.,  
 RA Sims M., Shaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,  
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,  
 RA Watson R., Watson A., Weinstock L., Wilkinston-Sproat J.,  
 RA Whitham P.,

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans."  
 RL Nature 368:32-38(1994).

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DR EMBL; Z22151; CAAB01B2.1; -.

DR PIR; S40937; SA0937.

DR WormPep; ZK632.5; CE00422.

KW Hypothetical protein.

SQ SEQUENCE 824 AA; 95726 MW; 05074058F5B73919 CRC64;.

Query Match 93.8%; Score 30; DB 1; Length 824;  
 Best Local Similarity 100.0%; Pred. No. 64; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7

Db 206 GFYRN 210

RESULT 15  
 XPC\_MOUSE STANDARD; PRT; 900 AA.  
 AC P51612; P54732; STANDARD;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DE DNA-repair Protein complementing XP-C cells homolog (Xeroderma  
 DB pigmentosum group C complementing protein homolog) (p125).  
 GN XPC.  
 OS Mus musculus (Mouse).  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TAXID=10099;  
 RN [1] SEQUENCE FROM N.A.  
 RX MEDLINE=96184849; PubMed=6604333;  
 RA Li L.; Peterson C.; Legerzki R.;  
 RT "Sequence of the mouse XPC cDNA and genomic structure of the human  
 XPC gene.";  
 RL Nucleic Acids Res. 24:1026-1028(1996).  
 RN [2] SEQUENCE OF 28-587 FROM N.A.  
 RX STRAIN=129/Sv;  
 RX MEDLINE=95405465; PubMed=7675084;  
 RA Sands A.T.; Abuin A.; Sanchez A.; Conti C.J.; Bradley A.;  
 RT "High susceptibility to ultraviolet-induced carcinogenesis in mice

RT lacking XPC.";  
 RL Nature 377:162-165(1995).  
 CC -!- FUNCTION: Involved in DNA excision repair. May play a part in DNA  
 CC damage recognition and/or in altering chromatin structure to  
 CC allow access by damage-processing enzymes.  
 CC -!- SUBUNIT: HETEROODIMER OF A 125 kDa SUBUNIT (P125) AND OF A  
 CC 58 kDa SUBUNIT (P88).  
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -!- SIMILARITY: Belongs to the XPC family.  
 CC  
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 CC  
 DR EMBL; U27398; AAC52500.1; -.  
 DR PIR; U40005; AAA822720.1; -.  
 DR MGD; MGI:103557; xpc.  
 DR GO:0006289; P:nucleotide-excision repair; IMP.  
 DR InterPro; IPR04583; Rad4.  
 DR pfam; PF03835; Rad4; 1.  
 DR TIGRFAMS; TIGR00605; rad4; 1.  
 DR DNA repair; DNA-binding; Nuclear protein.  
 DR CONFLICT 28 30 AVN -> CSD (IN REF. 2).  
 FT CONFLICT 53 53 S -> L (IN REF. 2).  
 FT CONFLICT 67 67 L -> F (IN REF. 2).  
 FT CONFLICT 70 70 L -> S (IN REF. 2).  
 DR RG -> TP (IN REF. 2).  
 FT CONFLICT 134 135 EVIDENT -> GVHD7 (IN REF. 2).  
 FT CONFLICT 165 170 S -> N (IN REF. 2).  
 FT CONFLICT 181 181 S -> N (IN REF. 2).  
 FT CONFLICT 187 187 S -> N (IN REF. 2).  
 FT CONFLICT 190 190 R -> S (IN REF. 2).  
 FT CONFLICT 192 192 P -> L (IN REF. 2).  
 FT CONFLICT 342 345 GSXRA -> AKP (IN REF. 2).  
 FT CONFLICT 367 367 R -> S (IN REF. 2).  
 FT CONFLICT 428 428 R -> C (IN REF. 2).  
 FT CONFLICT 467 467 C -> S (IN REF. 2).  
 FT CONFLICT 584 584 X -> E (IN REF. 2).  
 SQ SEQUENCE 900 AA; 9573/7FCB36DC15DD CRC64;

Query Match 93.8%; Score 30; DB 1; Length 900;  
 Best Local Similarity 100.0%; Pred. No. 70; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7  
 Db 182 GFYRN 186

Search completed: September 24, 2004, 07:34:58  
 Job time : 4.43158 secs



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## OM protein - protein search, using sw model

Run on: September 24, 2004, 07:28:32 ; Search time 7.29474 Seconds

(without alignments)

302.770 Million cell updates/sec

Perfect score: US-09-498-556C-79

Sequence: 1 XXGFYRN 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Q8lt75 arabiidopsis

Database : SPREMBBL2\_556C-79

1: sp\_archea:\*

2: sp\_bacteria:\*

3: sp\_fungi:\*

4: sp\_human:\*

5: sp\_invertebrate:\*

6: sp\_mammal:\*

7: sp\_micr:

8: sp\_organelle:\*

9: sp\_phage:\*

10: sp\_plant:\*

11: sp\_rabbit:\*

12: sp\_virus:\*

13: sp\_vertebrate:\*

14: sp\_unclassified:\*

15: sp\_virus:\*

16: sp\_bacteriap:\*

17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	30	93.8	77	16	Q8X3Q1	Q8x3Q1 escherichia
2	30	93.8	88	16	Q8FIE2	Q8fie2 escherichia
3	30	93.8	91	5	Q16938	Q16938 ancylostoma
4	30	93.8	102	5	Q9e2V8	Q9e2V8 ancylostoma
5	30	93.8	110	16	Q9KVV8	Q9Kvv8 streptomyce
6	30	93.8	113	16	Q82H68	Q82H68 streptomyce
7	30	93.8	134	16	P74345	P74345 synchocystis
8	30	93.8	154	5	Q8TPB8	Q8tpb8 oesophagostomus
9	30	93.8	158	2	Q44490	Q44490 anaerobium
10	30	93.8	172	16	Q9A2A6	Q9a2a6 caudobacter
11	30	93.8	178	8	Q9PAJ9	Q9paJ9 catenaria
12	30	93.8	182	16	Q7V9J4	Q7v9j4 prochlorococcus
13	30	93.8	184	5	Q9VGJ2	Q9vgj2 drosophila
14	30	93.8	184	5	Q9E723	Q9e723 drosophila
15	30	93.8	191	10	Q8L803	Q8l803 triticeum
16	30	93.8	216	17	Q8TNS2	Q8tns2 methanosc

Q8die9 synechococcus  
 Q8yq65 anaerobium sp  
 Q8gmr5 synchococcus  
 Q8uzb5 grapevine f  
 Q9hpv4 halobacteri  
 Q8ntl4 corynebacter  
 Q8fsu2 corynebacter  
 Q8t19 pyrobaculum  
 Q8c2V6 mus musculu  
 Q9bkk3 lucilia cup  
 Q9veyo drosophil  
 Q01482 caenorhabdi  
 Q9tl53 leishmania  
 Q9c8j9 arabiidopsis  
 Q8edg2 shewellina  
 Q9p868 sacharomyces  
 Q9p6k0 schizosaccharomyces  
 Q9dc65 mus musculu  
 Q8azn8 bacillus  
 Q8a6n8 bacillus  
 Q9j58 mus musculu  
 Q8grx1 arabiidopsis  
 Q91xx0 mus musculu  
 Q8zz12 pyrobaculum  
 Q86468 rhodobacter  
 Q9nl27 ciona intes  
 Q7vpM4 haemophilus  
 Q8gtz8 arabiidopsis  
 Q9lt75 arabiadopsis

SEQUENCE FROM N.A.

STRAIN=O157:H7 / EDL933 / ATCC 700927;

MEDIUM=1074935; Published: 2001-05-11;

Perna N.T., Plunkett G. III, Burland V., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirpatrick H.A.,

Possai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grobbeck E.J., Davis N.W., Lim A., Dimalauna E.T., Potamusis K.,

Apoaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7,"

RT Nature 409:529-533 (2000);

RL EMBL, AB005327; ARG5934.1;

DR PIR: B85684; B85685.

KW Hypothetical protein; Complete proteome;

SQ SEQUENCE 77 AA; 8087 MW; F8D56712A58545E CRC64;

Query Match 93.8%; Score 30; DB 16; Length 77;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYN 7

DB 15 GFYN 19

## ALIGNMENTS

RESULT 1	Q8X3Q1	PRELIMINARY;	PRT;	77 AA.
	ID Q8X3Q1;			
	AC Q8X3Q1;			
	DT 01-MAR-2002 (TREMBLrel. 20; Last sequence update)			
	DT 01-MAR-2002 (TREMBLrel. 20; Last annotation update)			
	DT 01-JUN-2003 (TREMBLrel. 24; Last annotation update)			
	DE HYPOTHETICAL PROTEIN z1836.			
	GN Z1836			
	OS Escherichia coli O157:H7.			
	OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;			
	OC Enterobacteriaceae; Escherichia.			
	OX NCBI_TaxID:8334; RN [1];			

SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDIUM=1074935; Published: 2001-05-11;
RA Perna N.T., Plunkett G. III, Burland V., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirpatrick H.A.,
RA Possai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalauna E.T., Potamusis K.,
RA Apoaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7,"
RL Nature 409:529-533 (2000);
DR EMBL, AB005327; ARG5934.1;
DR PIR: B85684; B85685.
KW Hypothetical protein; Complete proteome;
SQ SEQUENCE 77 AA; 8087 MW; F8D56712A58545E CRC64;
Query Match 93.8%; Score 30; DB 16; Length 77;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GFYN 7
DB 15 GFYN 19



RA	Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., Rabinowitz B., Rajandream M.A., Ruberford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Taylor K., Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J., Hopwood D. A.	DT 01-JUN-2003 (TREMBLrel. 24; Last annotation update)
RT	"Complete genome sequence of the model actinomycete Streptomyces coelicolor A3 (2)."	DE Hypothetical protein sir1628.
RL	Nature 417:141-147(2002).	GN SIR1628.
DR	EMBL; AL939115; CAB0971.1; -.	OS Synechocystis sp. (strain PCC 6803).
KW	Hypothetical protein; Complete proteome; Complementary proteome; Bacteria; Cyanobacteria; Chroococcales; Synechocystis.	OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
SEQUENCE	110 AA; 10831 MW; 0893.F052.B8EAF0A CRC64;	NCBI_TaxID=1148;
SQ		RN [1]
Query Match	93.8%; Score 30; DB 16; Length 110;	RP SEQUENCE FROM N.A.
Best Local Similarity	100.0%; Pred. No. 76;	RX MEDLINE#97061201; PubMed=8905231;
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RA Kaneo T.; Sato S.; Kotani H.; Tanaka A.; Asanizu E.; Nakamura Y.; Miyajima N.; Hirosewa M.; Sugiyama M.; Sasamoto S.; Kimura T.; Hosouchi T.; Matsuo A.; Muraki A.; Nakazaki N.; Narita K.; Okumura S.; Shimpo S.; Takeuchi C.; Wada T.; Watanabe A.; Yamada M.; Yasuda M.; Tabata S.; RT "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
QY	3 GFYRN 7	RT
Db	51 GFYRN 55	RT DNA Res. 3:109-116(1995); DR EMBL; D00914; BAA18439.1; -.
RESULT 6		DR PTR; S76180; S76180.
Q82H68	PRELIMINARY; PRT; 113 AA.	KW HYPOTHETICAL PROTEIN; Complete proteome.
AC	Q82H68	SQ SEQUENCE 134 AA; 14545 MW; 7B541.E80FB43D10 CRC64;
DT	01-JUN-2003 (TREMBLrel. 24; Created)	Query Match 93.8%; Score 30; DB 16; Length 134;
DT	01-JUN-2003 (TREMBLrel. 24; Last sequence update)	Best Local Similarity 100.0%; Pred. No. 93;
DT	01-JUN-2003 (TREMBLrel. 24; Last annotation update)	Mismatches 0; Indels 0; Gaps 0;
DE	Hypothetical protein.	NCBI_TaxID=6180;
GN	SAV3678.	RN RESULT 8
OS	Streptomyces avermitilis.	Q8ITP8 PRT; 154 AA.
OC	Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;	AC Q8ITP8 PRELIMINARY;
OC	Streptomyces; Streptomyceae; Streptomyces.	AC Q8ITP8 PRELIMINARY;
OX	NCBI_TaxID=33903;	AC Q8ITP8 PRELIMINARY;
RN	[1]	AC Q8ITP8 PRELIMINARY;
RP	SEQUENCE FROM N.A.	AC Q8ITP8 PRELIMINARY;
RC	STRAIN:MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;	AC Q8ITP8 PRELIMINARY;
RX	MEDLINE#21471403; PubMed=11572948;	AC Q8ITP8 PRELIMINARY;
RA	Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osono T., RA Kikuchi H., Shiba T., Sakaki Y., Hattori M., RA Genome sequence of an industrial microorganism, Streptomyces avermitilis: deducing the ability of producing secondary metabolites.";	AC Q8ITP8 PRELIMINARY;
RA	RP RIBOTAXONOMY: 21:526-531(2003).	AC Q8ITP8 PRELIMINARY;
DR	EMBL; AP005036; BAC71390.1; -.	AC Q8ITP8 PRELIMINARY;
KW	Hypothetical protein; Complete proteome.	AC Q8ITP8 PRELIMINARY;
SEQUENCE	113 AA; 11204 MW; CF49EEB26F5236DE CRC64;	AC Q8ITP8 PRELIMINARY;
SQ		AC Q8ITP8 PRELIMINARY;
Query Match	93.8%; Score 30; DB 16; Length 113;	AC Q8ITP8 PRELIMINARY;
Best Local Similarity	100.0%; Pred. No. 78;	AC Q8ITP8 PRELIMINARY;
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AC Q8ITP8 PRELIMINARY;
QY	3 GFYRN 7	AC Q8ITP8 PRELIMINARY;
Db	51 GFYRN 55	AC Q8ITP8 PRELIMINARY;
RESULT 7		AC Q8ITP8 PRELIMINARY;
P74345		AC Q8ITP8 PRELIMINARY;
ID		AC Q8ITP8 PRELIMINARY;
AC	P74345; P74445;	AC Q8ITP8 PRELIMINARY;
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)	AC Q8ITP8 PRELIMINARY;
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)	AC Q8ITP8 PRELIMINARY;
Query Match	93.8%; Score 30; DB 5; Length 154;	AC Q8ITP8 PRELIMINARY;
Best Local Similarity	100.0%; Pred. No. 1.1e+02;	AC Q8ITP8 PRELIMINARY;
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AC Q8ITP8 PRELIMINARY;
QY	3 GFYRN 7	AC Q8ITP8 PRELIMINARY;
Db	64 GFYRN 68	AC Q8ITP8 PRELIMINARY;
RESULT 9		AC Q44490 PRELIMINARY;
ID		AC Q44490 PRELIMINARY;
AC		AC Q44490 PRELIMINARY;
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)	AC Q44490 PRELIMINARY;

AC Q44490; DT 01-NOV-1996 (TREMBLrel. 01, Created) DB 01-JUN-2003 (TREMBLrel. 01, Last sequence update) OS Anabaena variabilis. OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena . RN [1] RP SEQUENCE FROM N.A. STRAIN=ATCC 29413; PubMed=7568132; RX MEDLINE=96016168; RT "A second nitrogenase in vegetative cells of a heterocyst-forming cyanobacterium."; Proc. Natl. Acad. Sci. U.S.A. 92:9358-9362(1995). RN [2] RP SEQUENCE FROM N.A. STRAIN=ATCC 29413; RA Thiel T., Lyons E. M., Erker J.C.; Submitted (FEB-1916) to the EMBL/GenBank/DBJ databases. DR InterPro; IPR004382; DUF269; Pfam; PF03270; DUF269; 1. DR PRODom; PD008304; DUF269; 1. SQ SEQUENCE 158 AA; 17791 MW; D157EBF59C36FEBD CRC64;

Query Match 93.8%; Score 30; DB 2; Length 158; Best Local Similarity 100.0%; Pred. No. 1.1e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7 Db 35 GFYRN 39

RESULT 10

Q9A2A6 ID Q9A2A6\_ PRELIMINARY; PRT; 172 AA. AC Q9A2A6; DT 01-JUN-2001 (TREMBLrel. 17, Created) DB 01-JUN-2003 (TREMBLrel. 17, Last sequence update) OS Hypothetical protein CC3660. CAulobacter crescentus. OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteria; OC Cauibacteriae; Caulobacter. RN [1] RP SEQUENCE FROM N.A. STRAIN=ATCC 19089 / CB15; MEDLINE=21173698; PubMed=11259647; RA Nieman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E., RA Bisen J.V., Heideberg J.F., Alley M.R.K., Chia N., Maddock J.R., RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., RA DeBoy R.T., Dodson R.J., Durkin A.S., Smit J., Craven M.B., Haft D.H., RA Kolonay J.F., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., White O., RA Salzberg S.L., Ventner J.C., Shapiro L., Fraser C.M.; RA Complete genome sequence of Caulobacter crescentus.; RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001). EMBL; AE006024; AACR25622.1; -. DR PIR; B87703; B87703. TIGR; CC3660; -. KW Hypothetical protein; Complete proteome. SQ SEQUENCE 172 AA; 18425 MW; 5D52E712F406F6A CRC64;

Query Match 93.8%; Score 30; DB 16; Length 172; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7

RESULT 11

Q9TA49 ID Q9TA49\_ PRELIMINARY; PRT; 178 AA. AC Q9TA49; DT 01-MAY-2000 (TREMBLrel. 13, Created) DB 01-JUN-2003 (TREMBLrel. 13, Last sequence update) DE ORF178. GN ORF178. OS Mitochondrion. Eukaryote; stramenopiles; Bicosoecida; Cafeteriae; Cafeteria. NCBI\_TaxID=33653; RN [1] RP SEQUENCE FROM N.A. RA Burger G.; RT "The mitochondrial genome of Cafeteria roenbergensis."; RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases. DR GO:0005739; ARF05739; C:mitochondrion; IEA. KW Mitochondrion. SEQUENCE 178 AA; 21418 MW; 00F69B2FC8461362 CRC64;

Query Match 93.8%; Score 30; DB 8; Length 178; Best Local Similarity 100.0%; Pred. No. 1.2e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7 Db 109 GFYRN 113

RESULT 12

Q7V9J4 ID Q7V9J4\_ PRELIMINARY; PRT; 182 AA. AC Q7V9J4; DT 01-OCT-2003 (TREMBLrel. 25, Created) DB 01-OCT-2003 (TREMBLrel. 25, Last sequence update) DE Predicted metal-dependent protease fused to Zn ribbon domain. GN PRO1839. OS Prochlorococcus marinus SS120, Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae; Prochlorococcus. NCBI\_TaxID=1219; RN [1] RP SEQUENCE FROM N.A. RC SPBAIN=SARG / CCMP 1375 / SS120; RX MEDLINE=2280154; PubMed=12917486; RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M., RA Barbe V., Duprat S., Galperin M.Y., Koorn E.V., Le Gall F., RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., RA Wolf Y.I., Hess W.R.; RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxygenic phototrophic genome."; RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003). DR EMBL; AE01166; AAQ0083.1; -. XW Protease; Complete proteome. SEQUENCE 182 AA; 20809 MW; 3D010CB5E5E0B7F6 CRC64;

Query Match 93.8%; Score 30; DB 16; Length 182; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7

RESULT 13

Q7V9J4 ID Q7V9J4\_ PRELIMINARY; PRT; 182 AA. AC Q7V9J4; DT 01-OCT-2003 (TREMBLrel. 25, Created) DB 01-OCT-2003 (TREMBLrel. 25, Last sequence update) DE Predicted metal-dependent protease fused to Zn ribbon domain. GN PRO1839. OS Prochlorococcus marinus SS120, Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae; Prochlorococcus. NCBI\_TaxID=1219; RN [1] RP SEQUENCE FROM N.A. RC SPBAIN=SARG / CCMP 1375 / SS120; RX MEDLINE=2280154; PubMed=12917486; RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M., RA Barbe V., Duprat S., Galperin M.Y., Koorn E.V., Le Gall F., RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., RA Wolf Y.I., Hess W.R.; RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxygenic phototrophic genome."; RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003). DR EMBL; AE01166; AAQ0083.1; -. XW Protease; Complete proteome. SEQUENCE 182 AA; 20809 MW; 3D010CB5E5E0B7F6 CRC64;

Query Match 93.8%; Score 30; DB 16; Length 182; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 44 GFYRN 48



Fri Sep 24 08:54:05 2004

us-09-498-556c-79.sep04.rsp

Page 6

Db 67 GFYRN 71

Search completed: September 24, 2004, 07:30:25  
Job time : 10.2947 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
 Run on: September 24, 2004, 07:30:36 ; Search time 4.34737 Seconds  
 (without alignments)  
 83.127 Million cell updates/sec

Title: US-09-498-556C-79  
 Perfect score: 32  
 Sequence: 1 XXGFTYN 7  
 Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

389414

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

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 6: /cgm2\_6/peodata/2/iaa/backfiles1.pep:  
 \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	30	93.8	5	2	US-09-465-380-70	Sequence 70, App1
2	30	93.8	5	2	US-08-377-70	Sequence 70, App1
3	30	93.8	5	2	US-08-386-359-70	Sequence 70, App1
4	30	93.8	5	2	US-08-461-265-70	Sequence 70, App1
5	30	93.8	5	2	US-08-634-641-70	Sequence 70, App1
6	30	93.8	5	3	US-09-249-411-70	Sequence 70, App1
7	30	93.8	5	3	US-09-249-472-70	Sequence 70, App1
8	30	93.8	5	3	US-09-249-451-70	Sequence 70, App1
9	30	93.8	5	3	US-08-309-455-70	Sequence 70, App1
10	30	93.8	5	3	US-09-249-461-70	Sequence 70, App1
11	30	93.8	5	3	US-08-634-541-70	Sequence 70, App1
12	30	93.8	5	4	US-09-249-473-70	Sequence 70, App1
13	30	93.8	7	2	US-08-465-380-79	Sequence 79, App1
14	30	93.8	7	2	US-08-486-397-79	Sequence 79, App1
15	30	93.8	7	2	US-08-486-399-79	Sequence 79, App1
16	30	93.8	7	2	US-08-461-365-79	Sequence 79, App1
17	30	93.8	7	3	US-08-634-541-79	Sequence 79, App1
18	30	93.8	7	3	US-09-249-471-79	Sequence 79, App1
19	30	93.8	7	3	US-09-249-472-79	Sequence 79, App1
20	30	93.8	7	3	US-09-249-451-79	Sequence 79, App1
21	30	93.8	7	3	US-08-609-455-79	Sequence 79, App1
22	30	93.8	7	3	US-09-249-461-79	Sequence 79, App1
23	30	93.8	7	3	US-09-249-448-79	Sequence 79, App1
24	30	93.8	7	4	US-09-249-473-79	Sequence 79, App1
25	30	93.8	78	2	US-08-465-380-47	Sequence 47, App1
26	30	93.8	78	2	US-08-486-397-47	Sequence 47, App1
27	30	93.8	78	2	US-08-486-399-47	Sequence 47, App1

#### ALIGNMENTS

RESULT 1  
 US-08-461-380-70  
 Sequence 70, Application US/08465380  
 Patent No. 5,863,894  
 GENERAL INFORMATION:  
 APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
 APPLICANT: Joris H.L. Mensens, Marc J. Lauwersys,  
 APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
 APPLICANT: Yannick G.J. Gansmans, Matthew Moyle,  
 APPLICANT: Peter W. Bergum  
 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Suite 4700  
 STATE: Los Angeles  
 COUNTY: California  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: Storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/465,380  
 FILING DATE: June 5, 1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 213/268  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 488-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 70:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 FRAGMENT TYPE: internal fragment  
 US-08-465-380-70

RESULT 2  
 Query Match Similarity 93.8%; Score 30; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; ;

Qy	3 GFYRN 7					
Dy	1 GFYRN 5					

---

RESULT 2  
 US-08-486-397-70  
 Sequence 70, Application US/084B6397  
 Patent No. 5866542  
 GENERAL INFORMATION:  
 APPLICANT: George P. Vlaasuk, Patric H. Stanssens,  
 Yves R. Laroche, Laurent S. Jespers,  
 Marc J. Lauweleys,  
 Joris H.L. Mensens, Peter W. Bergum, Matthew Moyle,  
 Yannick G.J. Gansmans,  
 TITLE OF INVENTION: NEMATOIDE-EXTRACTED ANTICOAGULANT  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C., DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/486,399  
 FILING DATE: June 5, 1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 213/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 481-1600  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 70:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 FRAGMENT TYPE: internal fragment  
 US-08-486-399-70

Query Match Similarity 93.8%; Score 30; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; ;

Qy	3 GFYRN 7					
Dy	1 GFYRN 5					

---

RESULT 4  
 US-08-461-965-70  
 Sequence 70, Application US/08461965  
 Patent No. 5872998  
 GENERAL INFORMATION:  
 APPLICANT: George P. Vlaasuk, Patric H. Stanssens,  
 Yves R. Laroche, Laurent S. Jespers,  
 Marc J. Lauweleys,  
 Joris H.L. Mensens, Peter W. Bergum, Matthew Moyle,  
 Yannick G.J. Gansmans,  
 TITLE OF INVENTION: NEMATOIDE-EXTRACTED ANTICOAGULANT  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street

STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 ZIP: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: Storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 CURRENT APPLICATION NUMBER: US/08/461,965  
 FILING DATE: June 5, 1995  
 CLASSIFICATION: 510  
 PRIOR APPLICATION NUMBER: 08/326,110  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 210/243  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 70:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: Internal fragment  
 US-08-461-965-70

Query Match 93.8%; Score 30; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 3e+05; Indels 0; Gaps 0;

Qy 3 GFYRN 7  
 Db 1 GFYRN 5

## RESULT 5

US-08-634-641-70  
 Sequence 70, Application US/08634641  
 Patent No. 5955294

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George P.  
 APPLICANT: Stanssens, Patrick Eric Hugo  
 APPLICANT: Mensens, Joris Hilda Lieven  
 APPLICANT: Lauwers, Marc Joseph  
 APPLICANT: Laroche, Yves Rene  
 APPLICANT: Jespers, Laurent Stephane  
 APPLICANT: Gansmans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew  
 APPLICANT: Bergum, Peter W.  
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible

## RESULT 6

US-08-634-641-70  
 Sequence 70, Application US/09249471  
 Patent No. 6043441

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 APPLICANT: Stanssens, Patrick Eric Hugo  
 APPLICANT: Mensens, Joris Hilda Lieven  
 APPLICANT: Lauwers, Marc Joseph  
 APPLICANT: Laroche, Yves Rene  
 APPLICANT: Jespers, Laurent Stephane  
 APPLICANT: Gansmans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew  
 APPLICANT: Bergum, Peter W.  
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Suite 4700  
 STATE: Los Angeles  
 COUNTRY: California  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible

COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/249,471  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/809,455  
 FILING DATE: April 17, 1997  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/446,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 70:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal fragment  
 US-09-249-471-70

Query Match Score 30; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy	3 G <sub>1</sub> F <sub>2</sub> Y <sub>3</sub> R <sub>4</sub> N <sub>5</sub>	3 G <sub>1</sub> F <sub>2</sub> Y <sub>3</sub> R <sub>4</sub> N <sub>5</sub>
Db	1 G <sub>1</sub> F <sub>2</sub> Y <sub>3</sub> R <sub>4</sub> N <sub>5</sub>	1 G <sub>1</sub> F <sub>2</sub> Y <sub>3</sub> R <sub>4</sub> N <sub>5</sub>

RESULT 7  
 US-09-249-472-70  
 Sequence 70, Application US/09249472  
 Patent No. 6046318  
 GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 APPLICANT: Stansens, Patrick Eric Hugo  
 APPLICANT: Messens, Joris Hilda Lieven  
 APPLICANT: Lauverays, Marc Joseph  
 APPLICANT: Laroche, Yves René  
 APPLICANT: Jespers, Laurent Stephane  
 APPLICANT: Ganssemans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew W.  
 APPLICANT: Bergum, Peter W.  
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT  
 TITLE OF INVENTION: PROTEIN  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/249,472  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/809,455  
 FILING DATE: April 17, 1997  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/446,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 70:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal fragment  
 US-09-249-472-70

Query Match Score 30; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy	3 G <sub>1</sub> F <sub>2</sub> Y <sub>3</sub> R <sub>4</sub> N <sub>5</sub>	3 G <sub>1</sub> F <sub>2</sub> Y <sub>3</sub> R <sub>4</sub> N <sub>5</sub>
Db	1 G <sub>1</sub> F <sub>2</sub> Y <sub>3</sub> R <sub>4</sub> N <sub>5</sub>	1 G <sub>1</sub> F <sub>2</sub> Y <sub>3</sub> R <sub>4</sub> N <sub>5</sub>

RESULT 8  
 US-09-249-451-70  
 Sequence 70, Application US/09249451  
 Patent No. 608497  
 GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 APPLICANT: Stansens, Patrick Eric Hugo  
 APPLICANT: Messens, Joris Hilda Lieven  
 APPLICANT: Lauverays, Marc Joseph  
 APPLICANT: Laroche, Yves René  
 APPLICANT: Jespers, Laurent Stephane  
 APPLICANT: Ganssemans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew W.  
 APPLICANT: Bergum, Peter W.  
 APPLICANT: Lyon & Lyon  
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT  
 TITLE OF INVENTION: PROTEIN  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION NUMBER: US/09/249,451  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/809,455  
FILING DATE: April 17, 1997  
APPLICATION NUMBER: PCT/US95/13231  
.FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal fragment  
US-09-249-451-70

Query Match 93.8%; Score 30; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GRYN 7  
Db 1 GRYN 5

RESULT 9  
US-08-809-455-70  
Sequence 70, Application US/0809455  
Patent No. 6030916  
GENERAL INFORMATION:  
APPLICANT: Viasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Lacoste, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganssemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Bergum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/809,455  
FILING DATE: April 17, 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal fragment  
US-08-809-455-70

Query Match 93.8%; Score 30; DB 3; Length 5;  
Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GRYN 7  
Db 1 GRYN 5

RESULT 10  
US-09-249-461-70  
Sequence 70, Application US/09249461  
Patent No. 6096577  
GENERAL INFORMATION:  
APPLICANT: Viasuk, George Phillip  
APPLICANT: Stanssens, Patrick Eric Hugo  
APPLICANT: Messens, Joris Hilda Lieven  
APPLICANT: Lauwereys, Marc Josef  
APPLICANT: Lacoste, Yves Rene  
APPLICANT: Jespers, Laurent Stephane  
APPLICANT: Ganssemans, Yannick Georges Jozef  
APPLICANT: Moyle, Matthew  
APPLICANT: Bergum, Peter W.  
TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS:  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/249,461  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/809,455  
 FILING DATE: April 17, 1997  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORM FOR SEQ ID NO: 70:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal fragment  
 US-09-249-461-70

Query Match 93.8%; Score 30; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy	3 GFYRN 7		3 GFYRN 7
Db	1 GFYRN 5		1 GFYRN 5

RESULT 11  
 US 09-249-448-70

Sequence 70, Application US/09249448  
 Patent No. 612,435  
 GENERAL INFORMATION  
 APPLICANT: Vlasiuk, George Phillip  
 APPLICANT: Stanssens, Patrick Eric Hugo  
 APPLICANT: Messens, Joris Hilda Lieven  
 APPLICANT: Lauwers, Marc Joseph  
 APPLICANT: Laroche, Yves Rene  
 APPLICANT: Jespers, Laurent Stephane  
 APPLICANT: Gansmans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew  
 APPLICANT: Bergun, Peter W.  
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT

RESULT 12  
 US-09-249-473-70

Sequence 70, Application US/09249473  
 Patent No. 653,429  
 GENERAL INFORMATION  
 APPLICANT: Vlasiuk, George Phillip  
 APPLICANT: Stanssens, Patrick Eric Hugo  
 APPLICANT: Messens, Joris Hilda Lieven  
 APPLICANT: Lauwers, Marc Joseph  
 APPLICANT: Laroche, Yves Rene  
 APPLICANT: Jespers, Laurent Stephane  
 APPLICANT: Gansmans, Yannick Georges Jozef  
 APPLICANT: Moyle, Matthew  
 APPLICANT: Bergun, Peter W.  
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT

APPLICANT: Bergum, Peter W.  
 TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
 TITLE OF INVENTION: INHIBITORS AND ANTIKOAGULANT  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 SUITE: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/249,473  
 FILING DATE:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/809,455  
 FILING DATE: April 17, 1997  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 213/268  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 79:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal fragment  
 INFORMATION FOR SEQ ID NO: 70:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal fragment  
 US-09-249-473-70

Query Match 93.8%; Score 30; DB 4; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

RESULT 13  
 US-08-465-380-79  
 GENERAL INFORMATION:  
 Sequence 79, Application US/08465380  
 Patent No. 58665894

RESULT 13  
 US-08-465-380-79  
 GENERAL INFORMATION:  
 Sequence 79, Application US/08465380  
 Patent No. 58665894

Query 3 GFYRN 7  
 Db 1 GFYRN 5

Query 3 GFYRN 7  
 Db 3 GFYRN 7

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
 TITLE OF INVENTION: PROTEIN  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/465,380  
 FILING DATE: June 5, 1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 213/268  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 79:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal fragment  
 FEATURE:  
 OTHER INFORMATION: Xaa in locations 1 and 2  
 OTHER INFORMATION: is an amino acid, provided  
 that at least one Xaa is Glu or  
 ASP.  
 US-08-465-380-79

Query Match 93.8%; Score 30; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

RESULT 14  
 US-08-465-397-79  
 General Information:  
 Sequence 79, Application US/08486397  
 Patent No. 5866542

GENERAL INFORMATION:  
 APPLICANT: George P. Vlasuk, Patric H. Stanssens,  
 APPLICANT: Joris H.L. Mensens, Marc J. Lauwers,  
 APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
 APPLICANT: Yannick G.J. Gansmans, Matthew Moyle,  
 APPLICANT: Peter W. Bergum  
 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT  
 NUMBER OF SEQUENCES: 357  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Suite 4700  
 CITY: Los Angeles

STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/486,397  
 FILING DATE: June 5, 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 213/270  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 79:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 FRAGMENT TYPE: internal fragment  
 FRAGMENT:  
 PEPTIDE:  
 INFORMATION FOR SEQ ID NO: 79:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 FRAGMENT TYPE: peptide  
 FRAGMENT TYPE: internal fragment  
 FEATURE:  
 OTHER INFORMATION: Xaa in locations 1 and 2  
 OTHER INFORMATION: is an amino acid, provided  
 OTHER INFORMATION: that at least one Xaa is Glu or  
 OTHER INFORMATION: Asp.  
 US-08-486-397-79

Query Match 93.8%; Score 30; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7  
 Db 3 GFYRN 7

Search completed: September 24, 2004, 07:50:01  
 Job time : 5.34737 secs

RESULT 15  
 US-08-486-399-79  
 Sequence 79, Application US/08486399  
 Patent No. 586543  
 GENERAL INFORMATION:  
 APPLICANT: George P. Vlasuk, Patrick H. Stanssens,  
 APPLICANT: Joris H.L. Mensens, Marc J. Lauwers,  
 APPLICANT: Yves R. Laroche, Laurent S. Jespers,  
 APPLICANT: Yannick G.J. Gansmans, Matthew Moyle,  
 APPLICANT: Peter W. Bergum  
 TITLE OF INVENTION: NEMATOXB-EXTRACTED ANTICOAGULANT  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 STREET: Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 MEDIUM TYPE: storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: September 24, 2004, 07:35:06 ; Search time 60:2737 Seconds

(without alignments) 37.345 Million cell updates/sec

Title: US-09-498-556C-79

Perfect score: 32 - XXGYRN 7

Sequence: Scoring table: BLOSUM62

GapP 10.0 , Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published\_Applications\_AA.\*

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7: /cgn2_6/prodata/1/pubpaas/US08_PUBCOMB.pep:*
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18: /cgn2_6/prodata/1/pubpaas/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Description
Length	DB ID	%	
1	30	93.8	5 10 US-09-498-272-70
2	30	93.8	7 Sequence 70, App1
3	30	93.8	7 Sequence 79, App1
4	30	93.8	8 Sequence 47, App1
5	30	93.8	82 Sequence 25, App1
6	30	93.8	82 Sequence 19, App1
7	30	93.8	83 Sequence 52, App1
8	30	93.8	84 Sequence 50, App1
9	30	93.8	84 Sequence 51, App1
10	30	93.8	84 Sequence 59, App1
11	30	93.8	87 Sequence 24, 9825,
12	30	93.8	89 Sequence 48, App1
13	30	93.8	91 Sequence 128, App1
14	30	93.8	92 Sequence 263, 776,
15	30	93.8	102 Sequence 27, App1
			Sequence 24, App1

TITLE OF INVENTION: NEMATOIDE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN

NUMBER OF SEQUENCES: 336

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ST ORGE  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C., DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498,272  
 FILING DATE: 04 Feb-2000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995

#### ALIGNMENTS

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RESULT 1
US-09-498-272-70
; Sequence 70, Application US/09498272
; Publication No. US20030113890A1
; GENERAL INFORMATION:
; APPLICANT: Vlasuk, George Phillip
; Strassens, Patrick Eric Hugo
; Massens, Joris Hilda Lieven
; Lauwers, Marc Josef
; Laroche, Yves René
; Jaspers, Laurent Stéphane
; Gangsemans, Yannick Georges Jozef
; Moyle, Matthew
; Bergum, Peter W.

TITLE OF INVENTION: NEMATOIDE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN
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16	30	93.8	113 Sequence 11215, A
17	30	93.8	138 Sequence 1934, App1
18	30	93.8	138 Sequence 1934, App1
19	30	93.8	149 Sequence 13009, A
20	30	93.8	161 Sequence 65, App1
21	30	93.8	162 Sequence 63, App1
22	30	93.8	162 Sequence 64, App1
23	30	93.8	171 Sequence 62, App1
24	30	93.8	185 Sequence 35, App1
25	30	93.8	192 Sequence 14775, App1
26	30	93.8	240 Sequence 159958, App1
27	30	93.8	243 Sequence 43449, A
28	30	93.8	252 Sequence 36701, A
29	30	93.8	260 Sequence 3828, App1
30	30	93.8	268 Sequence 43, App1
31	30	93.8	354 Sequence 9303, App1
32	30	93.8	359 Sequence 9498, App1
33	30	93.8	359 Sequence 15415, A
34	30	93.8	361 Sequence 78000, A
35	30	93.8	361 Sequence 15783, A
36	30	93.8	361 Sequence 16164, A
37	30	93.8	362 Sequence 17731, A
38	30	93.8	382 Sequence 120180, A
39	30	93.8	475 Sequence 65, App1
40	30	93.8	533 Sequence 5, App1
41	30	93.8	533 Sequence 75, App1
42	30	93.8	623 Sequence 10-024-599-238442, App1
43	30	93.8	795 Sequence 1, App1
44	30	93.8	795 Sequence 3, App1
45	30	93.8	795 Sequence 13, App1

APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,385  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 955-0440  
 TELEX: (213) 955-0440  
 INFORMATION FOR SEQ ID NO: 70:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal fragment  
 SEQUENCE DESCRIPTION: SEQ ID NO: 70:  
 US-09-498-72-70

Query Match 93.8%; Score 30; DB 10; Length 5;

Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;

Qy 3 GFYRN 7  
 |||||  
 Db 1 GFYRN 5

RESULT 2  
 US-09-498-272-79  
 / Sequence 79, Application US/09498272  
 / Publication No. US20030113890A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Vlasuk, George Phillip  
 Stanssens, Patrick Eric Hugo  
 Messens, Joris Hilda Lieven  
 Lauwers, Marc Joseph  
 Laroch, Yves Rene  
 Jespers, Laurent Stephane  
 Ganssens, Yannick Georges Jozef  
 Moy, Matthew  
 Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
 INHIBITORS AND ANTICOAGULANT  
 PROTEIN  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C., DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498-272  
 FILING DATE: 04-Feb-2000  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/15231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,385  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEX: (213) 955-0440  
 INFORMATION FOR SEQ ID NO: 79:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 7 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal fragment  
 FEATURE:  
 OTHER INFORMATION: Xaa in locations 1 and 2  
 is an amino acid, provided  
 that at least one Xaa is Glu or  
 ASP.  
 SEQUENCE DESCRIPTION: SEQ ID NO: 79:  
 US-09-498-272-79

Query Match 93.8%; Score 30; DB 10; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;

RESULT 3  
 US-09-498-272-47  
 / Sequence 47, Application US/09498272  
 / Publication No. US20030113890A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Vlasuk, George Phillip  
 Stanssens, Patrick Eric Hugo  
 Messens, Joris Hilda Lieven  
 Lauwers, Marc Joseph  
 Laroch, Yves Rene  
 Jespers, Laurent Stephane  
 Ganssens, Yannick Georges Jozef  
 Moy, Matthew  
 Bergum, Peter W.  
 Bergum, Peter W.  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C., DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498-272  
 FILING DATE: 04-Feb-2000  
 PRIOR APPLICATION DATA:

COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498-272  
 FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 79 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancyclostoma caninum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 47:  
 US-09-498-272-47

Query Match 93.8%; Score 30; DB 10; Length 78;  
 Best Local Similarity 100.0%; Pred. No. 55;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;

Qy 3 GFYRN 7  
 Db 54 GFYRN 58

RESULT 4  
 US-09-498-272-25  
 Sequence 25, Application US/09498272  
 Publication No. US2003011389041

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip Hugo  
 Messens, Joris Hilda Lieven  
 Lauwers, Marc Josef  
 Laroche, Yves Rene  
 Jaspers, Laurent Stephane  
 Gansmans, Yannick Georges Jozef  
 Moyle, Matthew Peter W.  
 Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN

NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 storage

COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498-272  
 FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 25:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 82 amino acids  
 TYPE: amino acid  
 TOPOLOGY: Linear  
 MOLECULE TYPE: Peptide

ORIGINAL SOURCE:  
 ORGANISM: Ancyclostoma ceylanicum

US-09-498-272-25

SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
 Query Match 93.8%; Score 30; DB 10; Length 82;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0;  
 Gaps 0;

Qy 3 GFYRN 7  
 Db 51 GFYRN 55

RESULT 5  
 US-09-498-272-49  
 Sequence 49, Application US/09498272  
 Publication No. US2003011389041

GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip Hugo  
 Messens, Joris Hilda Lieven  
 Lauwers, Marc Josef  
 Laroche, Yves Rene  
 Jaspers, Laurent Stephane  
 Gansmans, Yannick Georges Jozef  
 Moyle, Matthew Peter W.  
 Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTI COAGULANT PROTEIN

NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071

STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,272  
FILING DATE: 04-Feb-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REDOCKET NUMBER: 216/270  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 82 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancyclostoma ceylanicum  
SEQUENCE DESCRIPTION: SEQ ID NO: 49;  
US-09-498-272-49

Query Match 93.8%; Score 30; DB 10; Length 82;  
Best Local Similarity 100.0%; Pred. No. 58;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GFYRN 7  
Db 51 GFYRN 55

RESULT 6  
US-09-498-272-52  
Sequence 52, Application US/09498272  
GENERAL INFORMATION:  
APPLICANT: Viasuk, George Phillip  
Mestens, Patrick Eric Hugo  
Lauwereys, Marc Joseph  
Laroche, Yves René  
Ganssens, Laurent Stephane  
Moyse, Matthew  
Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT  
NUMBER OF SEQUENCES: 356  
CORRESPONDENCE ADDRESS: Lyon & Lyon  
ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,272  
FILING DATE: 04-Feb-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/466,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 83 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancyclostoma duodenale  
US-09-498-272-52

RESULT 7  
US-09-498-272-50  
Sequence 50, Application US/09498272  
GENERAL INFORMATION:  
APPLICANT: Viasuk, George Phillip  
Mestens, Patrick Eric Hugo  
Lauwereys, Marc Joseph  
Laroche, Yves René  
Ganssens, Laurent Stephane  
Moyse, Matthew  
Jespers, Laurent Stephane  
Ganssens, Yannick Georges Jozef  
Bergum, Peter W.  
Noyle, Matthew  
Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT  
PROTEIN  
INHIBITORS AND ANTICOAGULANT

NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498,272  
 FILING DATE: 04-Feb-2000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 SOFTWARE: Word Perfect 5.1  
 APPLICATION NUMBER: US/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 50:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 50:  
 US-09-498-272-50

Query Match 93.8%; Score 30; DB 10; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7  
 DB 56 GFYRN 60

RESULT 8  
 US-09-498-272-51  
 Sequence 51; Application US/09498272  
 Publication No. US2003013890A1  
 GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 Scansens, Patrick Eric Hugo  
 Meessens, Joris Hilda Lieven  
 Lauwers, Marc Josef  
 La Roche, Yves Rene  
 Jespers, Laurent Stephane  
 Gansmans, Yannick Georges Jozeef  
 Moyle, Matthew  
 Bergum, Peter W.

RESULT 9  
 US-09-498-272-59  
 Sequence 59; Application US/09498272  
 Publication No. US2003013890A1  
 GENERAL INFORMATION:  
 APPLICANT: Vlasuk, George Phillip  
 Scansens, Patrick Eric Hugo  
 Meessens, Joris Hilda Lieven  
 Lauwers, Marc Josef  
 La Roche, Yves Rene  
 Jespers, Laurent Stephane  
 Gansmans, Yannick Georges Jozeef  
 Moyle, Matthew  
 Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT  
 NUMBER OF SEQUENCES: 356  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Lyon & Lyon  
 STREET: 633 West Fifth Street  
 Suite 4700  
 CITY: Los Angeles  
 STATE: California  
 COUNTRY: U.S.A.  
 ZIP: 90071  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498,272  
 FILING DATE: 04-Feb-2000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/13231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEFAX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 50:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 84 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 51:  
 US-09-498-272-51

Query Match 93.8%; Score 30; DB 10; Length 84;  
 Best Local Similarity 100.0%; Pred. No. 59;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7  
 DB 56 GFYRN 60

Ganssmans, Yannick Georges Jozef  
Moyle, Matthew  
Bergum, Peter W.

TITLE OF INVENTION: NEONATO-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOGULANT PROTEIN

NUMBER OF SEQUENCES: 3566

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C., DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,272  
FILING DATE: 04-Feb-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 216/270

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 935-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 59:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 84 amino acids  
TYPE: amino acid  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Anyclostoma caninum

SEQUENCE DESCRIPTION: SEQ ID NO: 59:  
US-09-498-272-59

Query Match 93.8%; Score 30; DB 10; length 84;  
Best Local Similarity 100.0%; Pred. No. 59;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GYTRN 7  
Db 55 GYTRN 59

RESULT 10  
US-10-424-599-249825  
Sequence 249825, Application US/10424599  
Publication No. US0040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovacic David K  
APPLICANT: Zhou Yihua

NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEX: (213) 955-0440  
 INFORMATION FOR SEQ ID NO: 48:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 89 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma ceylanicum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 48:  
 us-09-498-272-48

Query Match 93.8%; Score 30; DB 10; Length 89;  
 Best Local Similarity 100.0%; Pred. No. 63;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 GFYRN 7  
 Db 61 GFYRN 65

RESULT 12  
 US-09-498-272-128  
 ; Sequence 128, Application US/09498272  
 ; Publication No. US20030113891A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vilasik, George Phillip  
 ; Stanssens, Patrick Eric Hugo  
 ; Messens, Joris Hilda Lieven  
 ; Lauwereys, Marc Joseph  
 ; Laroche, Yves Rene  
 ; Jespers, Laurent Stephane  
 ; Ganssens, Yannick Georges Jozef  
 ; Moyle, Matthew  
 ; Bergum, Peter W.  
 ; TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE  
 ; INHIBITORS AND ANTICOAGULANT  
 ; PROTEIN  
 ; NUMBER OF SEQUENCES: 356  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Lyon & Lyon  
 ; STREET: 633 West Fifth Street  
 ; Suite 4700  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071  
 COMPUTER READEABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 storage  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: IBM P.C. DOS 5.0  
 SOFTWARE: Word Perfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/498,272  
 FILING DATE: 04-Feb-2000  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/113231  
 FILING DATE: October 17, 1995  
 APPLICATION NUMBER: 08/486,399  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/486,397  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/465,380  
 FILING DATE: June 5, 1995  
 APPLICATION NUMBER: 08/461,965  
 FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/326,110  
 FILING DATE: October 18, 1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: BIGGS, SUZANNE L.  
 REGISTRATION NUMBER: 30,158  
 REFERENCE/DOCKET NUMBER: 216/270  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (213) 489-1600  
 TELEX: (213) 955-0440  
 TELEX: 67-3510  
 INFORMATION FOR SEQ ID NO: 128:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 91 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 ORIGINAL SOURCE:  
 ORGANISM: Ancylostoma caninum  
 SEQUENCE DESCRIPTION: SEQ ID NO: 128:  
 us-09-498-272-128  
 Query Match 93.8%; Score 30; DB 10; Length 91;  
 Best Local Similarity 100.0%; Pred. No. 64;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 GFYRN 7  
 Db 62 GFYRN 66

RESULT 13  
 US-10-424-599-263776  
 ; Sequence 263776, Application US/10424599  
 ; Publication No. US20040031072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa Thomas J  
 ; APPLICANT: Kovalic David K  
 ; APPLICANT: Zhou Yinhua  
 ; APPLICANT: Cao Yongwei  
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53223)B  
 ; CURRENT APPLICATION NUMBER: US/10/424,599  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 285684  
 ; SEQ ID NO: 263776  
 ; LENGTH: 92  
 ; TYPE: PRT  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_80209C.1.pep  
 US-10-424-599-263776  
 Query Match 93.8%; Score 30; DB 12; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 65;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 GFYRN 7  
 Db 19 GFYRN 23

RESULT 14  
 US-09-498-272-27  
 ; Sequence 27, Application US/09498272  
 ; Publication No. US20030113890A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vlaubek, George Phillip  
 ; Stanssens, Patrick Eric Hugo  
 ; Messens, Joris Hilda Lieven  
 ; Lauwereys, Marc Joseph  
 ; Laroche, Yves Rene  
 ; Jespers, Laurent Stephane  
 ; Ganssens, Yannick Georges Jozef  
 ; Bergum, Peter W.

Gansmans, Yannick Georges Jozef  
Moyle, Matthew W.  
Bergum, Peter W.

TITLE OF INVENTION: NEANTODE-EXTRACTED SERINE PROTEASE INHIBITORS AND ANTICOAGULANT PROTEIN

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/498,272  
FILING DATE: 04-Feb-2000

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/13231  
FILING DATE: October 17, 1995  
APPLICATION NUMBER: 08/486,399  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/486,397  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/465,380  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/461,965  
FILING DATE: June 5, 1995  
APPLICATION NUMBER: 08/326,110  
FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFFERENCE/DOCKET NUMBER: 216/270

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 102 amino acids  
TYPE: amino acid  
TOPOLOGY: Linear  
MOLECULE TYPE: Peptide  
ORIGINAL SOURCE:  
ORGANISM: Ancylostoma duodenale

SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-498-272-27

Query Match 3 GFYRN 7 Score 30; DB 10; Length 102;  
Best Local Similarity 100.0%; Pred. No. 72;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 3 GFYRN 7 Score 30; DB 10; Length 108;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15  
US-09-498-272-24  
Sequence 24, Application US/09498272  
Publication No. US2003011389A1  
GENERAL INFORMATION:  
APPLICANT: Vlaert, George Phillip  
Stanssens, Patrick Eric Hugo  
Messens, Joris Hilda Lieven

Qy 3 GFYRN 7  
Db 80 GFYRN 84

Search completed: September 24, 2004, 08:10:04  
Job time : 61.2737 secs

Gencore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: September 24, 2004, 07:28:32 ; Search time 9.68421 Seconds  
 116.704 Million cell updates/sec

Title: US-09-498-556C-357

Perfect score: 11

Sequence: 1 LXXX 4

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2001s:\*

4: geneseqp2002s:\*

5: geneseqp2003s:\*

6: geneseqp2003bs:\*

7: geneseqp2004s:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Description
		ID	Length
1	9	81.8	Aaw84193 Peptide C
2	9	81.8	Aaw48182 Conantoki
3	9	81.8	Aaw49964 Conantoki
4	9	81.8	AAG79019 Amino aci
5	9	81.8	AAM51957 PSA antib
6	9	81.8	AAM51953 PSA antib
7	9	81.8	AAC24457 BONTA N-
8	9	81.8	AAB14417 C-terminal
9	9	81.8	AAB20561 Soybean d
10	9	81.8	Abu13761 Novel hum
11	9	81.8	ABJ36682 G protein
12	9	81.8	ABJ36606 G protein
13	9	81.8	ADC17690 Type IV C
14	9	81.8	ADC97797 MAPK-2 g
15	9	81.8	Aar03446 Accessory
16	9	81.8	Aar48999 Sequence
17	9	81.8	Aar50136 Ovine Gro
18	9	81.8	Aar50134 Ovine Gro
19	9	81.8	Aar50135 Ovine Gro
20	9	81.8	AAR77333 Human apo
21	9	81.8	AAM00252 Subtilis
22	9	81.8	AAM00251 Subtilis
23	9	81.8	Aaw5696 Cyclic pe
24	9	81.8	Aaw09695 Cyclic pe
25	9	81.8	Aaw37317 Mammalian

## ALIGNMENTS

26	9	81.8	AAV51458 AAV VP3 d
27	9	81.8	Aae05461 MASP sub
28	9	81.8	Aae11109 Tryptic P
29	9	81.8	Aae11144 Chymotryp
30	9	81.8	Aam51956 PSA antib
31	9	81.8	Aam51952 PSA antib
32	9	81.8	ABG77841 Targettin
33	9	81.8	ABE26308 Human rBP
34	9	81.8	ABP55342 Spinacia
35	9	81.8	ABP55341 Curcurbita
36	9	81.8	ABP75051 Proteome
37	9	81.8	ABR55078 MMP subst
38	9	81.8	ACI7431 Type IV C
39	9	81.8	Aar46808 Phytase d
40	9	81.8	Aar50143 Ovine gro
41	9	81.8	Aar50142 Ovine gro
42	9	81.8	Aar50141 Ovine gro
43	9	81.8	Aar55741 dsDNA-dep
44	9	81.8	Aar90511 Hybridoma
45	9	81.8	AAB74602 3-methylic

RESULT 1	Aaw84193	standard; peptide; 3 AA.
ID	XX	
AC	XX	
DT	25-MAR-1999	(first entry)
XX	XX	Peptide comprising a proteinase site.
DE	XX	
XX	XX	Proteinase site; bone morphogenetic fusion protein; bone binding site;
KW	XX	bone morphogenetic protein; transforming growth factor beta;
KW	XX	active fragment; wound healing; bone growth.
XX	XX	Unidentified.
OS	XX	
XX	XX	
PN	W09855137-A1.	
PD	10-DEC-1998.	
XX	XX	9BMO-US011189.
PP	02-TUN-1998;	
XX	PR 03-TUN-1997;	97US-00868452.
XX	XX	(NINNI/ ) NIMNI M.E.
PA	PA	(HALL/ ) HALL F.L.
PA	PA	(WU/L/ ) WU L.
PA	PA	(HANB/ ) HAN B.
PA	PA	(SHOR/ ) SHORS E.C.
XX	XX	Nimni ME, Hall FL, Wu L, Han B, Shors EC;
PI	XX	WPI: 1999-059875/05.
XX	DR	Claim 8; Page 34: 64pp; English.
XX	XX	The present peptide represents a proteinase site used in the creation of the bone morphogenetic fusion protein. The bone morphogenetic fusion protein may contain some or all of the following elements: a proteinase site, a ECM/bone binding site, a second proteinase site, and a bone morphogenetic active fragment. The fusion proteins of the invention also includes proteins that have transforming growth factor beta active fragments instead of bone morphogenetic protein active fragments. The bone morphogenetic

fusion proteins can be used for enhancing wound healing or bone growth

XX Sequence 3 AA;

Query Match Score 9; DB 2; Length 3;  
Best Local Similarity 81.8%; Pred. No. 1.3e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
Db 1 LTR 3

RESULT 2  
ID AAW48182 standard; peptide; 4 AA.  
AAW48182;  
AC XX  
DT 30-JUN-1998 (first entry)  
DE Conantokin peptide derivative.  
XX Conantokin; predatory cone snail; treatment; neurologic disorder;  
KW psychiatric disorder; anticonvulsant; neuroprotective;  
KW analgesic; HIV infection; ophthalmic indication; memory; learning defect;  
KW cognitive defect.  
XX Synthetic.

Key Location/Qualifiers  
PH PT /note= "gamma-carboxyglutamic acid"  
XX WO9803541-A1.  
XX 2S-JAN-1998.  
XX 21-JUL-1997; 97WO-US012618.  
XX 22-JUL-1996; 96US-00684742.  
XX (UTAH ) UNIV UTAH RES FOUND.  
PA (COGN-) COGNETIX INC.  
XX Abogadie FC, Cruz LJ, Olivera BM, Walker C, Colledge C;  
PI Hilliard DR, Jimenez E, Layer RT, Zhou L, Shen GS, McCabe RT;  
PI Rivier JE;  
XX WPI; 1998-120694/11.  
XX New conantokin peptide(s) - useful for e.g. treating neurologic or  
psychiatric disorders, or the management of pain.  
Claim 15: Page 98; 122pp; English.

XX The present sequence is a conantokin peptide derivative, which can be  
used to treat neurologic and psychiatric disorders, e.g. as an  
anticonvulsant, neuroprotective or analgesic agent. Neurologic and  
psychiatric disorders include epilepsy, convulsions, neurotoxic injury  
associated with conditions of hypoxia, anoxia or ischaemia, which  
typically follow stroke, cerebrovascular accident, brain or spinal cord  
trauma, myocardial infarct, physical trauma, drowning, suffocation,  
peripheral asphyxia or hypoglycaemic events, neurodegeneration  
(associated with Alzheimer's disease, senile dementia, Amyotrophic  
lateral Sclerosis, Multiple Sclerosis, Parkinson's disease, Huntington's  
disease, Down's Syndrome, Korsakoff's disease, schizophrenia, AIDS  
dementia, multi-infarct dementia, Binswanger dementia and neuronal damage  
associated with uncontrolled seizures), chemical toxicity (such as  
addiction, and morphine, opiate, opioid and barbiturate tolerance), pain  
(acute, chronic, migraine), anxiety, major depression, manic-depressive  
illness, obsessive-compulsive disorder, schizophrenia and mood disorders  
(such as bipolar disorder, unipolar depression, dysthymia and seasonal

CC effective disorder) and dystonia (movement disorder), sleep disorder,  
CC muscle relaxation and urinary incontinence. The peptide can also be used  
CC to treat HIV infection, ophthalmic indication and memory, learning or  
CC cognitive defects

XX SQ Sequence 4 AA;

Query Match Score 9; DB 2; Length 4;  
Best Local Similarity 81.8%; Pred. No. 1.3e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
Db 1 LAR 3

RESULT 3  
ID AAW49964 standard; peptide; 4 AA.  
XX AAW49964;  
AC XX  
DT 30-JUN-1998 (first entry)  
DE Conantokin peptide derivative.  
XX Conantokin; predatory cone snail; treatment; neurologic disorder;  
KW psychiatric disorder; anticonvulsant; neuroprotective;  
KW analgesic; HIV infection; ophthalmic indication; memory; learning defect;  
KW cognitive defect.  
XX OS Synthetic.  
PH Key Location/Qualifiers  
FT Modified-site 4  
XX WO9803189-A1.  
XX PN 29-JAN-1998.  
XX PD 29-JUL-1997; 97WO-US012652.  
XX PF 22-JUL-1996; 96US-00684750.  
XX PR 06-DEC-1996; 96US-00762377.  
XX PA (COGN-) COGNETIX INC.  
XX Mccabe RT, Zhou L, Layer RT;  
PI WPI; 1998-120469/11.  
XX DR XX  
PT Use of conantokin peptide(s) - for treating disorders involving excessive  
PT excitation of nerve cells by excitatory amino acids or agonists of the N-  
methyl-D-aspartate receptor.  
XX PS Claim 27; Page 69; 122pp; English.  
XX The present sequence is a conantokin peptide derivative, which can be  
used to treat neurologic and psychiatric disorders, e.g. as an  
anticonvulsant, neuroprotective or analgesic agent. Neurologic and  
psychiatric disorders include epilepsy, convulsions, neurotoxic injury  
associated with conditions of hypoxia, anoxia or ischaemia, which  
typically follow stroke, cerebrovascular accident, brain or spinal cord  
trauma, myocardial infarct, physical trauma, drowning, suffocation,  
peripheral asphyxia or hypoglycaemic events, neurodegeneration  
(associated with Alzheimer's disease, senile dementia, Amyotrophic  
lateral Sclerosis, Multiple Sclerosis, Parkinson's disease, Huntington's  
disease, Down's Syndrome, Korsakoff's disease, schizophrenia, AIDS  
dementia, multi-infarct dementia, Binswanger dementia and neuronal damage  
associated with uncontrolled seizures), chemical toxicity (such as  
addiction, and morphine, opiate, opioid and barbiturate tolerance), pain  
(acute, chronic, migraine), anxiety, major depression, manic-depressive  
illness, obsessive-compulsive disorder, schizophrenia and mood disorders  
(such as bipolar disorder, unipolar depression, dysthymia and seasonal

CC illness; obsessive-compulsive disorder, schizophrenia and mood disorders  
 CC (such as bipolar disorder, unipolar depression, dysthymia and seasonal  
 CC effective disorder) and dystonia (movement disorder), sleep disorder,  
 CC muscle relaxation and urinary incontinence. The peptide can also be used  
 CC to treat HIV infection, ophthalmalic indication and memory, learning or  
 CC cognitive defects

XX SQ Sequence 4 AA;

Query Match 81.8%; Score 9; DB 2; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX

RESULT 4  
 AAG79019 standard; peptide; 4 AA.

XX ID AAG79019

AC AAG79019;

XX DT 10-DEC-2001 (first entry)

XX DB Amino acid sequence of conantokin R domain III.

XX XX

KW Conantokin; cone snail; nerve cell excitation; NMDA receptor; epilepsy;  
 KW N-methyl-D-aspartate receptor; pain; Psychiatric disorder;  
 KW neurotoxic injury; hypoxia; anoxia; ischemia; neurodegeneration;  
 KW chemical toxicity; addiction; drug craving; psychiatric disorder;  
 KW anxiety; depression; obsessive compulsive disorder; schizophrenia;  
 KW mood disorder; ophthalmalic disorder; neurological disorder; dystonia;  
 KW sleep disorder; muscle relaxation; prostatic carcinoma; pro-kallikrein 2;  
 KW cognition enhancement; urinary incontinence;  
 KW HIV infection.

XX OS Conus radiatus.

XX FH Key Location/Qualifiers

FT Modified-site 4 /note= "gamma-carboxyglutamic acid"

XX XX

PN US6277825-B1.

XX PD 21-AUG-2001.

XX PF 20-JUL-1999;

XX 99US-00357141.

XX PR 22-JUL-1996;

XX 96US-006B4750.

PR 06-DEC-1996;

XX 96US-00762377.

PR 21-JUL-1997;

XX 97WO-US01652.

PR 10-FEB-1999;

XX 99US-0014076.

PR 01-APR-1999;

XX 99US-00283277.

XX PA (UTAH ) UNIV UTAH RES FOUND.

PA (COGN-) COGNETIX INC.

XX PI Olivera BM, McIntosh JM, McCabe RT, Layer RT, Zhou L;

XX DR WPI; 2001-601377/68.

XX Use of conantokin peptide or its derivatives or a conantokin peptide

PT chimeras for treating disorders e.g. migraine.

XX Claim 9; Col 80; 60pp; English.

XX XX

AAG79012-43 and AAG790054-56 represent domains of conantokin peptides.

Conantokins differ from conotoxins, in that they contain gamma-carboxyglutamic acid. The conantokins are derived from the venom of cone snails. They are used for the treatment of disorders in which the pathophysiology involves excessive excitation of nerve cells by excitatory amino acids or agonist of N-methyl-D-aspartate (NMDA)

CC receptor. The conantokin peptides are used for the treatment of disorders  
 CC such as pain, neurologic or psychiatric disorders such as epilepsy; for  
 CC reducing neurotoxic injury associated with conditions of hypoxia, anoxia  
 CC or ischemia; for treating neurodegeneration; for creating chemical  
 CC toxicity such as addiction, drug craving, alcohol abuse, morphine, opioid  
 CC and barbiturate tolerance; for treating psychiatric disorders such as  
 CC anxiety, major depression, manic-depression illness, obsessive compulsive  
 CC disorder, schizophrenia or mood disorder; for treating ophthalmalic  
 CC disorder; for treating additional neurological disorders e.g. dystonia,  
 CC sleep disorder, muscle relaxation and urinary incontinence; for  
 CC memory/cognition enhancement; for treating HIV infection.

XX SQ Sequence 4 AA;

Query Match 81.8%; Score 9; DB 2; Length 4;

Best Local Similarity 66.7%; Pred. No. 1.3e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX

RESULT 4  
 AAG79019 standard; peptide; 4 AA;

XX ID AAG79019

AC AAG79019;

XX DT 10-DEC-2001 (first entry)

XX DB Amino acid sequence of conantokin R domain III.

XX XX

KW Conantokin; cone snail; nerve cell excitation; NMDA receptor; epilepsy;  
 KW N-methyl-D-aspartate receptor; pain; Psychiatric disorder;  
 KW neurotoxic injury; hypoxia; anoxia; ischemia; neurodegeneration;  
 KW chemical toxicity; addiction; drug craving; psychiatric disorder;  
 KW anxiety; depression; obsessive compulsive disorder; schizophrenia;  
 KW mood disorder; ophthalmalic disorder; neurological disorder; dystonia;  
 KW sleep disorder; muscle relaxation; prostatic carcinoma; pro-kallikrein 2;  
 KW human; antibody; immunogen.

XX OS Homo sapiens.

XX PN DE10032040-A1.

XX XX

PD 29-NOV-2001.

XX XX

PP 05-JUL-2000; 2000DE-01032040.

XX PR 24-MAY-2000; 2000DE-01025387.

XX XX

(HOFF ) ROCHE DIAGNOSTICS GMBH.

XX PA WPI; 2002-042633/06.

XX DR Disclosure; Page 11; 16pp; German.

XX XX

The present invention relates to an antibody specific for (-5,-6 and -7)-proPSA (prostate-specific antigen), but with no reactivity with (-4) or shorter forms of the protein. The antibody can be used to diagnose prostatic carcinoma and to detect human pro-kallikrein 2. The present sequence is a peptide which forms part of a peptide-containing immunogen described in the exemplification of the invention

XX PS Sequence 4 AA;

XX SQ Query Match 81.8%; Score 9; DB 5; Length 4;

Best Local Similarity 66.7%; Pred. No. 1.3e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

XX

QY 1 LXR 3

DB 1 LSR 3

RESULT 6	XX	16-NOV-2001;	2001WO-US044030.
AAM51953	PF		
ID AAM51953 ;	XX	17-NOV-2000;	2000US-0249540P.
AC XX	PR		
XX	XX	(ALLR ) ALLERGAN SALES INC.	
DT 01-FEB-2002 (first entry)	PA		
XX	XX	Steward LE, Spanoannis A,	Lin W, Aoki KR;
DE PSA antibody preparation immunogen Peptide #5.	PI		
XX	XX	WPI; 2002-479904/51.	
KW PSA; prostate-specific antigen; prostatic carcinoma; pro-kallikrein 2;	DR		
KW human; antibody; immunogen.	XX	Modified neurotoxin especially Clostridial toxins, useful for treating neuromuscular and autonomic nervous system disorder and pain, comprises structural modification to alter biological persistence of neurotoxin.	
XX	XX	Disclosure; Page 19; 55pp; English.	
OS Homo sapiens .	PS		
XX	XX	The invention related to modified neurotoxins especially Clostridial botulinum toxins with altered biological persistence. These toxins comprise a structural modification which is effective to alter the biological persistence. Modified neurotoxins of the invention are used for treating biological disorders which include neuromuscular disorder e.g. strabismus, blepharospasm, spasmodic torticollis (cervical dystonia), oromandibular dystonia and spasmodic dysphonia (laryngeal dystonia), autonomic nervous system disorders e.g. excessive salivation and sweating, asthma etc. and pain e.g. headache, muscular tension, neuralgia and neuropathy. The present sequence is botulinum toxin serotype A (BONT/A) N-glycosylation site. This peptide is derived from C botulinum	
PN DE10032040-A1.	PN		
XX	CC		
PD 29-NOV-2001.	CC		
XX	CC		
PP 05-JUL-2000;	CC		
2000DE-01032040.	CC		
XX	CC		
PR 24-MAY-2000;	CC		
2000DE-01025387.	CC		
XX	CC		
(HOFF ) ROCHE DIAGNOSTICS GMBH.	CC		
PA 2002-042633/06.	CC		
DR 2002-042633/06.	CC		
PT Antibody comprising specificity for some truncated forms of pro-prostate specific antigen, useful in immunoassays for differential diagnosis of prostatic carcinoma.	CC		
XX	CC		
PS Disclosure; Page 11; 16pp; German.	CC		
XX	CC		
CC The present invention relates to an antibody specific for (-5,-6 and -7) - proPSA (prostate specific antigen), but with no reactivity with (-4) or shorter forms of the protein. The antibody can be used to diagnose prostatic carcinoma and to detect human pro-kallikrein 2. The present sequence is a peptide which forms part of a peptide-containing immunogen described in the exemplification of the invention	CC		
XX	CC		
SQ Sequence 4 AA;	CC		
XX	CC		
Query Match 8	AAE14417		
Best Local Similarity 81.8%;	ID AAE14417 standard; peptide; 4 AA.		
Matches 2;	Length 4;		
CC Pred. No. 1.3e+06;	Score 9;	DB 5;	Length 4;
AC 0;	CC	66.7%;	Pred. No. 1.3e+06;
XX Mismatches 0;	CC	0;	Indels 0;
Db 1 LXR 3	CC	0;	Gaps 0;
Db 2 LTR 4	CC	0;	
XX	XX		
DT 26-MAR-2002 (first entry)	XX		
XX	XX		
DE C-terminal sequence of an arginine-containing peptide.	XX		
XX	XX		
AAE24457	XX		
ID AAE24457 standard; peptide; 4 AA.	XX		
XX	XX		
AC AAE24457;	XX		
XX	XX		
DT 04-OCT-2002 (first entry)	XX		
XX	XX		
DE BONT/A N-glycosylation site #1.	XX		
XX	XX		
Neurotoxin; biological persistence; blepharospasm; pain; therapy; neuromuscular disorder; cervical dystonia; oromandibular dystonia; spasmodic dysphonia; laryngeal dystonia; muscular tension; asthma; neuralgia; autonomic nervous system disorder; sweating; salivation; headache; neuropathy; botulinum toxin serotype A; BONT/A.	XX		
XX	XX		
Clostridium botulinum.	XX		
WO200240506-A2.	XX		
PD 23-MAY-2002.	XX		
(PURD ) PURDUE RES FOUND.	XX		
REGNIER F E.	PA (REGN/)		
PA (CHAK/)	XX		
CHAIRABORTY A B.	PR 05-MAY-2000;	2000US-0203227P.	
DORMDY S J.	PR 31-MAY-2000;	2000US-0208182P.	
(GENG/)	PR 31-MAY-2000;	2000US-0208312P.	
G'ENG M.	PA (GENG/)		
(JIIJ/)	PA (JIIJ/)		
JI J.	PA (JI J/)		

PA (RIGGS/) RIGGS L D.  
 PA (SIOMI/) SIOMA C S.  
 PA (WANG/) WANG S.  
 PA (ZHAN/) ZHANG X.  
 XX  
 PI Regnier FE, Chakraborty AB, Dormady SJ, G'eng M, Ji J, Riggs LD;  
 PI Sioma CS, Wang S, Zhang X;  
 XX DR WPI: 2002-089810/12.  
 XX PS Example 9; Page 73; 106pp; English.

PT Analyzing differences in protein content in protein samples, useful for  
 PT identifying protein(s) in a sample or multiple proteins in a single  
 complex mixture, by employing mass spectrometric analysis of signature  
 peptides.  
 XX  
 XX  
 CC The invention relates to analysing differences in protein content among  
 CC plural protein samples comprising employing mass spectrometric analysis  
 CC of proteolytic peptide fragments. The method comprises fragmenting at  
 CC least a first protein sample and a second protein sample to produce a  
 CC first peptide pool and a second peptide pool; isotopically labelling at  
 CC least a portion of the peptides in at least one of the pools so as to  
 CC permit resolution of otherwise identical peptides in the first and second  
 CC peptide pools by mass analysis; contacting peptides from at least a  
 CC portion of both of the peptide pools with a capture moiety to yield  
 CC affinity-selected peptides comprising an affinity ligand, where the  
 CC capture moiety selects for the affinity ligand; and analysing the  
 CC affinity-selected peptides by mass spectrometry to determine one or more  
 CC differences between the first and second samples. The method of the  
 CC invention is useful for identifying one or more proteins in the sample,  
 CC and is typically useful for identifying multiple proteins in a single  
 CC complex mixture. The method is also useful for quantifying proteins in a  
 CC complex or several samples. The advantages of the novel method are that it  
 CC is easier to separate peptides than proteins; native structure of the  
 CC protein does not have to be maintained during the analysis; structural  
 CC variants do not interfere, and putative proteins suggested from DNA  
 CC database can be recognised by using a signature peptide probe. The  
 present method permits identification of protein in a complex sample  
 without purifying the protein or obtaining its composite peptide  
 signature. The present sequence is C-terminal fragment of a  
 CC differentially acetylated arginine-containing peptide which is used to  
 CC generate fragment ions for distinguishing isobaric peptides  
 XX SQ Sequence 4 AA;

CC Query Match Score 9; DB 5; Length 4;  
 CC Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
 CC Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 CC PT 25-FEB-2003 (first entry)  
 CC DE Novel human transporter protein related peptide #4.  
 CC Homo sapiens.  
 CC US2002142381-P1.  
 CC XX PR 28-MAR-2001; 2001US-00818656.  
 CC PA (GONG/) GONG P.  
 CC PA (KETCHUM K A. (KETCHUM K A.  
 CC PA (DI FRANCESCO V. (DFRA/)  
 CC PA (BEASLEY E M. (BEAS/)  
 CC XX PD 28-FEB-2002.  
 CC XX PR 01-JUL-2002 (first entry)  
 CC DE Soybean diverged delta-9 fatty acid desaturase peptide #7.  
 CC KW soybean; diverged delta-9 fatty acid desaturase; enzyme; cellular lipid;  
 CC KW oil; transgenic plant; gene mapping; immunisation.  
 CC OS Glycine max.  
 CC PN WO200216565-A2.  
 CC XX PD 28-FEB-2002.

XX XX PF 22-AUG-2001; 2001WO-US026246.  
 XX PR 22-AUG-2000; 2000US-02269965.  
 XX PA (DUFIO ) DU PONT DE NEMOURS & CO E I.  
 XX PI Booth JR, Cahoon RE, Hitz WD, Kinney AJ, Yadav NS;  
 XX DR WPI; 2002-269353/31.  
 XX PS Claim 12; Page 48; 77pp; English.

CC The present invention relates to diverged delta-9 fatty acid desaturase  
 CC proteins and polynucleotides encoding such proteins. The nucleic acid  
 CC sequences may be used to increase the level of unsaturation in cellular  
 CC lipids including oil, in tissues when the enzyme is absent or rate-  
 CC limiting, to isolate cDNAs and genes encoding homologous proteins from  
 CC the same or other plant species and to create transgenic plants in which  
 CC the polypeptides are present at higher or lower levels than normal or in  
 CC cell types or developmental stages in which they are not normally found,  
 CC thus altering the level of mono-, poly- and unsaturated fatty acids in  
 CC those cells. They are useful as probes for genetic and physical gene  
 CC mapping and as markers, e.g. restriction fragment length polymorphism  
 CC (RFLP) markers. The peptides can be used to immunise animals to produce  
 CC antibodies specific for the peptides and proteins. The present sequence  
 CC is soybean diverged delta-9 fatty acid desaturase peptide (residues 256-  
 CC 259) sequence 4 AA;

XX SQ Sequence 4 AA;

Query Match Score 9; DB 5; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3  
 Db 2 LAR 4

RESULT 10  
 ABU13761  
 ID ABU13761 standard; Peptide: 4 AA.  
 XX AC ABU13761;  
 XX DT 25-FEB-2003 (first entry)  
 XX DE Novel human transporter protein related peptide #4.  
 XX KW Human; Gamma-aminobutyric acid; GABA; neurotransmitter transporter;  
 KW transgenic animal; ribozyme design; drug screening; gene therapy.  
 XX OS Homo sapiens.  
 XX PN US2002142381-P1.  
 XX PD 03-OCT-2002.  
 XX PP 28-MAR-2001; 2001US-00818656.  
 XX PR (GONG/) GONG P.  
 XX PA (KETCHUM K A. (KETCHUM K A.  
 XX PA (DI FRANCESCO V. (DFRA/)  
 XX PA (BEASLEY E M. (BEAS/)  
 XX XX

PI Gong F, Ketchum KA, Di Francesco V, Beasley EM;  
 XX  
 DR; 2003-102517/09.

XX Novel human transporter protein, related to gamma-aminobutyric acid  
 PT neurotransmitter transporter subfamily useful as model for developing  
 human therapeutic targets and serves as target for human therapeutics.  
 PT  
 PR 14-MAR-2001; 2001US-0275472P.  
 PR 11-MAY-2001; 2001US-00852910.  
 XX  
 PA (CUEB-B) CUE BIOTECH.

PS Disclosure; Page 45; 114PP; English.

XX The invention describes an isolated human transporter peptide (I) that is  
 CC related to the gamma-aminobutyric acid (GABA) neurotransmitter  
 CC transporter subfamily. (I) and the nucleic acid encoding it (II) can be  
 CC used as models for the development of human therapeutic targets and in  
 CC the identification of therapeutic proteins and serve as targets for the  
 CC development of human therapeutic agents that modulate transporter  
 CC activity. (I) is used to raise antibodies or to elicit another immune  
 CC response, as a reagent in assays designed to quantitatively determine  
 CC levels of the protein in biological fluids, and as markers for tissues in  
 CC which the corresponding protein is preferentially expressed. The  
 CC transporter proteins isolated from humans and their human/mammalian  
 CC orthologues serve as targets for identifying agents for use in mammalian  
 CC therapeutic applications, and biological assays related to transporter  
 CC proteins that are related to members of the GABA neurotransmitter  
 CC transporter subfamily. The proteins and peptides also provide a target  
 CC for diagnosing a disease or predisposition to disease mediated by the  
 CC peptide, and are useful for treating a disorder characterised by absence  
 CC of, inappropriate, unwanted or altered expression of the protein. The  
 CC antibodies are also useful for assessing normal and aberrant subcellular  
 CC localisation of cells in various tissues in an organism, in  
 CC pharmacogenomic analyses, for tissue typing and for inhibiting protein  
 CC function. (II) is useful for constructing recombinant vectors, host cells  
 CC and transgenic animals; for designing ribozymes; in drug screening; in  
 CC diagnostic assays for qualitative changes in gene expression,  
 CC particularly in qualitative changes that lead to pathology; in gene  
 CC therapy; and to detect mutations in genes encoding transporters. This is  
 CC the amino acid sequence of a polypeptide related to the novel human  
 CC aminobutyric acid (GABA) transporter related protein  
 XX  
 SQ Sequence 4 AA;

Query Match 81.8%; Score 9; DB 6; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3  
 Db 2 LTR 4

RESULT 11  
 ABJ36682 ID ABJ36682 standard; peptide; 4 AA.  
 XX  
 AC ABJ36682;  
 DT 01-MAY-2003 (first entry)

XX G protein coupled receptor related peptide SEQ ID No 5.

KW Nootropic; cardiotonic; antiarteriosclerotic; hypotensive; cyrostatic;  
 KW antihypertrophic; analgesic; antiasthmatic; antiinflammatory;  
 KW osteopathic; neuroprotective; anxiolytic; anorectic; lead compound;  
 KW G protein coupled receptor signaling inhibitor; GPCR; library;  
 KW high throughput screening assay; stroke; myocardial infarction;  
 KW restenosis; atherosclerosis; hypertension; cancer; infection; asthma;  
 KW septic shock; pain; allergic disorder; inflammatory bowel disease;  
 KW osteoporosis; obesity; psychotropic; neurological disorder; anxiety;  
 KW schizophrenia; Alzheimer's disease.  
 XX  
 OS Mammalia sp.  
 XX  
 PN WO200272778-A2.

SQ Sequence 4 AA;

Query Match 81.8%; Score 9; DB 6; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3  
 Db 1 LSR 3

RESULT 12  
 ABJ36806 ID ABJ36806 standard; peptide; 4 AA.  
 XX  
 AC ABJ36806;  
 DT 01-MAY-2003 (first entry)

XX G protein coupled receptor related peptide SEQ ID No 155.  
 KW Nootropic; cardiotonic; antiarteriosclerotic; hypotensive; cyrostatic;  
 KW antibacterial; analgesic; antiasthmatic; antiinflammatory;  
 KW osteopathic; neuroprotective; anxiolytic; anorectic; lead compound;  
 KW G protein coupled receptor signaling inhibitor; GPCR; library;  
 KW high throughput screening assay; stroke; myocardial infarction;  
 KW restenosis; atherosclerosis; hypertension; cancer; infection; asthma;  
 KW septic shock; pain; allergic disorder; inflammatory bowel disease;  
 KW osteoporosis; obesity; psychotropic; neurological disorder; anxiety;  
 KW schizophrenia; Alzheimer's disease.  
 XX  
 OS Unidentified.

XX KW blood-borne tumour.  
 PN XX Synthetic.  
 XX OS Homo sapiens.  
 PD XX OS  
 XX WO2003012122-A2.  
 PF 19-SEP-2002.  
 PR 14-MAR-2002; 2002WO-US007561.  
 PR 14-MAR-2001; 2001US-0275472P.  
 PR 11-MAY-2001; 2001US-00852910.  
 XX DR 26-JUL-2002; 2002WO-US023763.  
 PA (CUEB-) CUE BIOTECH.  
 XX PT (UNIV ) UNIV KANSAS MEDICAL CENT.  
 PI Gilchrist A, Hamm HE;  
 XX PT (SUND/ ) SUNDARAMOORTHY M.  
 PT (HUSD/ ) HUSDON B.  
 XX DR 27-JUL-2001; 2001US-0308523D.  
 PR 29-OCT-2001; 2001US-051289P.  
 PR 22-MAR-2002; 2002US-0166854P.  
 PR 03-JUN-2002; 2002US-0385362P.  
 PA (UNIV ) UNIV KANSAS MEDICAL CENT.  
 PI Sundaramoorthy M, Hudson B;  
 XX DR WPI; 2003-332730/31.  
 PT New polypeptide, useful for treating an angiogenesis-mediated disease or condition consisting of glaucoma or blood-borne tumors or for inhibiting basal lamina membrane formation in cell or tissue development.  
 PT PA (SUND/ ) SUNDARAMOORTHY M.  
 PT (HUSD/ ) HUSDON B.  
 XX PS Sundaramoorthy M, Hudson B;  
 XX DR WPI; 2003-332730/31.  
 PT The present invention describes a crystallised NC1 domain hexamer of type IV collagen (I). Also described: (1) a chimeric polypeptide; (2) a pharmaceutical composition comprising the polypeptide and a carrier; (3) inhibiting angiogenesis in tissue; (4) treating an angiogenesis-mediated disease or condition in a mammal; (5) inhibiting tumour metastasis or growth; (6) inhibiting basal lamina extracellular matrix in an animal tissue; (7) a crystal of an NC1 domain hexamer of type IV collagen; (8) identifying inhibitors of type IV collagen assembly; and (9) an inhibitor of type IV collagen assembly. A crystallised NC1 domain hexamer of type IV collagen (I) has cytostatic, antipsoriatic, antiandemic, ophthalmological, antiarteriosclerotic, antiulcer activities, and can be used as an inhibitor of angiogenesis, tumour growth, tumour metastasis, endothelial cell adhesion, endothelial cell proliferation, and basal lamina assembly. A (1) polypeptide can be used for treating an angiogenesis-mediated disease or condition consisting of glaucoma, sickle cell anaemia, ulcerative colitis, psoriasis, atherosclerosis, rheumatoid arthritis or blood-borne tumours or for inhibiting basal lamina membrane formation in cell or tissue development. The methods are useful for inhibiting angiogenesis in tissue, inhibiting tumour metastasis or growth, inhibiting endothelial cell interaction with the extracellular matrix in an animal tissue, and identifying inhibitors of type IV collagen assembly. The present sequence represents a peptide which is used in the exemplification of the present invention.

XX SQ Sequence 4 AA;  
 XX SQ Sequence 4 AA;  
 XX Query Match Best Local Similarity Score 9; DB 6; Length 4;  
 XX Matches 2; Conservative 66.7%; Pred. No. 1.3e+06;  
 XX Mismatches 0; Gaps 0;  
 XX DT 18-DEC-2003 (first entry).  
 DE Type IV collagen NC1 domain related peptide SEQ ID NO:295.  
 DE XX crystallised NC1 domain hexamer of type IV collagen;  
 DE KW angiogenesis inhibitor; angiogenesis-mediated disease;  
 DE KW tumour metastasis inhibitor; tumour growth inhibitor;  
 DE KW endothelial cell interaction inhibitor;  
 DE KW basal lamina membrane formation inhibitor; cytostatic; antipsoriatic;  
 DE KW antihaemiac; ophthalmological; antiarteriosclerotic; antiulcer;  
 DE KW endothelial cell adhesion inhibitor;  
 DE KW endothelial cell proliferation inhibitor; glaucoma; sickle cell anaemia;  
 DE KW ulcerative colitis; psoriasis; atherosclerosis; rheumatoid arthritis;

XX Qy 1 LXR 3  
 Db 2 LTR 4

RESULT 13  
 ADC17690  
 ID ADC17690 standard; peptide; 4 AA.  
 AC ADC17690;  
 XX DT 18-DEC-2003 (first entry).  
 DE Query Match Best Local Similarity Score 9; DB 7; Length 4;  
 DE Matches 2; Conservative 66.7%; Pred. No. 1.3e+06;  
 DE Mismatches 1; Gaps 0;

Qy 1 LXR 3  
 Db 1 LAR 3

RESULT 14  
 ADC9797  
 ID ADC97797 standard; peptide; 4 AA.  
 AC ADC97797;

DT 01-JAN-2004 (first entry)  
 XX MAPKK-2 gene regulatory peptide.  
 XX gene expression modulation; signalling molecule;  
 XX antiinflammatory; antiarthritic;  
 XX NF-kappaB/Rel protein inhibitor; antiinflammatory receptor.  
 XX cerebroprotective; cardiotropic; antibiotic; immunosuppressive;  
 XX dermatological; nephroprotective; NF-kappaB/Rel protein modulator;  
 XX inflammatory disease; arthritis; ischaemia; cerebrovascular disease;  
 XX ischaemic heart failure; arrhythmia; angiogenesis; autoimmune disease;  
 XX systemic lupus erythematosus; ulcerative colitis; Addison's disease;  
 XX Goodpasture's disease.  
 XX Synthetic.

XX WO2003029292-A2.  
 XX PD 10-APR-2003.  
 XX 04-OCT-2002; 2002WO-NL000639.  
 XX 04-OCT-2001; 2001EP-00203748.  
 PR 21-DEC-2001; 2001US-00028075.  
 XX (UTRO-) UNIV ROTTERDAM ERASMUS.  
 XX DR 2003-393380/37.  
 PI Khan NA, Benner R:  
 XX Disclosure; Page 35; 217pp; English.  
 PT Modulating gene expression in a cell, useful for treating acute or  
 PT chronic inflammatory diseases (e.g. arthritis), ischemic events or  
 PT autoimmune diseases, comprises providing the cell with a signaling  
 PT molecule.  
 XX PS Disclosure; Page 35; 217pp; English.  
 PT The present invention describes a method for modulating gene expression  
 PT comprising providing the cell with a signalling molecule.  
 PT comprising a peptide or its functional analogue. Also described: (1)  
 PT identifying or obtaining a signalling molecule comprising a peptide or  
 PT its functional derivative or analogue capable of modulating expression of  
 PT a gene in a cell; (2) a signalling molecule useful in modulating  
 CC expression of a gene in a cell and identifiable or obtainable by the  
 CC method of (1); and (3) an inhibitor of nuclear factor (NF)-kappaB/Rel  
 CC protein activation comprising a signalling molecule of (2). The  
 CC signalling molecule has antiinflammatory, antiarthritic,  
 CC cerebroprotective, cardiotropic, antibiotic, immunosuppressive,  
 CC dermatological and nephroprotective activities, and can be used as a NF-  
 CC kappaB/Rel protein modulator. The signalling molecule is useful for the  
 CC production of a pharmaceutical composition for the modulation of gene  
 CC expression by inhibiting NF-kappaB/Rel protein activation. The method is  
 CC useful for modulating gene expression, and for treating acute or chronic  
 CC inflammatory diseases (e.g. arthritis), ischaemic event including  
 CC cerebrovascular disease and ischaemic heart failure, arrhythmia,  
 CC angiogenesis, or autoimmune diseases (e.g. systemic lupus erythematosus,  
 CC ulcerative colitis, Addison's disease or Goodpasture's disease). The  
 CC present sequence represents a peptide used in the exemplification of the  
 present invention.  
 XX Sequence 4 AA:  
 SQ 81.8%; Score 9; DB 7; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query 1 LXR 3  
 Db 3 LAR 5

Search completed: September 24 2004, 07:34:20  
 Job time : 13.6842 secs

Query 1 LXR 3  
 Db 2 LAR 4

RESULT 15  
 AAR03446

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## OM protein - protein search, using sw model

Run on: September 24, 2004, 07:30:36 ; Search time 2.48421 Seconds  
 (without alignments)

83.127 Million cell updates/sec

Title: US-09-498-556c-357

Perfect score: 11

Sequence: 1 LRRX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database :

- Issued Patents AA:\*
  - 1: /cggn2\_6/picodata/2/iaaa/5A\_COMB\_pep:\*
  - 2: /cggn2\_6/picodata/2/iaaa/5B\_COMB\_pep:\*
  - 3: /cggn2\_6/picodata/2/iaaa/6A\_COMB\_pep:\*
  - 4: /cggn2\_6/picodata/2/iaaa/6B\_COMB\_pep:\*
  - 5: /cggn2\_6/picodata/2/iaaa/pc7tus\_COMB\_pep:\*
  - 6: /cggn2\_6/picodata/2/iaaa/backfiles1\_pep:\*

Pred. No. is the number of results Predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Description	Length	DB ID
1	9	81.8	Sequence 7, App1	3	US-08-470-837-7
2	9	81.8	Sequence 7, App1	3	US-08-468-452-7
3	9	81.8	Sequence 4, App1	4	US-08-388-405A-4
4	9	81.8	Sequence 36, App1	4	US-08-33A-36
5	9	81.8	Sequence 19, App1	4	US-09-142-078-19
6	9	81.8	Sequence 19, App1	4	US-09-357-141-19
7	9	81.8	Sequence 19, App1	4	US-09-533-899-19
8	9	81.8	Sequence 19, App1	4	US-09-142-080-19
9	9	81.8	Sequence 4, App1	4	US-09-486-283C-4
10	9	81.8	Sequence 355, App1	4	US-09-335-852-355
11	9	81.8	Sequence 12, App1	5	US-07-636-923A-12
12	9	81.8	Sequence 5, App1	5	US-08-317-264-5
13	9	81.8	Sequence 38, App1	5	US-08-456-840-38
14	9	81.8	Sequence 5, App1	5	US-08-672-511-5
15	9	81.8	Sequence 173, App1	5	US-07-759-181-173
16	9	81.8	Sequence 12, App1	5	US-08-061-192-12
17	9	81.8	Sequence 37, App1	5	US-08-460-313B-37
18	9	81.8	Sequence 38, App1	5	US-08-346-343B-38
19	9	81.8	Sequence 173, App1	5	US-08-175-263-173
20	9	81.8	Sequence 37, App1	5	US-08-398-038B-37
21	9	81.8	Sequence 38, App1	5	US-08-398-028B-38
22	9	81.8	Sequence 38, App1	5	US-08-286-407A-38
23	9	81.8	Sequence 173, App1	5	US-08-455-886-173
24	9	81.8	Sequence 37, App1	5	US-0-504-265B-37
25	9	81.8	Sequence 38, App1	5	US-08-504-265B-38
26	9	81.8	Sequence 12, App1	5	US-08-545-151-12
27	9	81.8	Sequence 7, App1	5	US-08-392-973A-7

## ALIGNMENTS

RESULT 1  
 US-08-470-837-7  
 Sequence 7, Application US-08470837  
 ; Patent No. 5800811  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Niimi, Marcel E.  
 ; APPLICANT: Hall, Frederick L.  
 ; APPLICANT: Tuan, Tai-Lan  
 ; APPLICANT: Wu, Lingtao  
 ; APPLICANT: Cheung, David T.  
 ; TITLE OF INVENTION: Transforming Growth Factor B Fusion  
 ; TITLE OF INVENTION: and  
 ; TITLE OF INVENTION: Their Use in Wound Healing  
 ; NUMBER OF SEQUENCES: 34  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Merchant & Gould  
 ; STREET: 11150 Santa Monica Boulevard, Suite 400  
 ; CITY: Los Angeles  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 90025-3395  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: FLOPPY disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/470,837  
 ; APPLICATION DATE:  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Sharf, Janice A.  
 ; REGISTRATION NUMBER: 34,051  
 ; REFERENCE/DOCKET NUMBER: 30630-1US01  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 310-445-1140  
 ; TELEFAX: 310-445-9031  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3 amino acids  
 ; TYPE:  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; US-08-470-837-7

Query Match 81.8%; Score 9; DB 1; Length 3;  
 Best Local Similarity 66.7%; Pred. No. 2.e+05;  
 Matches 2; Conservative 0; Gaps 0;  
 Indels 0; Mismatches 1;

Qy 1 LXR 3  
Db 1 LTR 3

RESULT 2  
US-08-868-452A-7  
Sequence 7, Application US/08868452C  
GENERAL INFORMATION:  
APPLICANT: Frederick L. Hall  
APPLICANT: Langtao Wu  
APPLICANT: Bo Han  
APPLICANT: Edwin Shors  
TITLE OF INVENTION: BONE MORPHOGENETIC PROTEINS AND THEIR FILE REFERENCE: 17972-11  
CURRENT APPLICATION NUMBER: US/08/868,452C  
CURRENT FILING DATE: 1997-06-03  
NUMBER OF SEQ ID NOS: 51  
SOFTWARE: FastSEQ for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 3  
TYPE: PRT  
ORGANISM: Human

US-08-868-452A-7

Query Match: Score 9; DB 4; Length 3;  
Best Local Similarity 66.7%; Pred. No. 2.9e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
Db 1 LTR 3

RESULT 3  
US-08-88-405A-4  
Sequence 4, Application US/08288405A  
PATENT NO. 5550009  
GENERAL INFORMATION:  
APPLICANT: Chandy, Ranjithara G.  
APPLICANT: Kalmann, Katalin  
APPLICANT: Chandy, Grischa  
APPLICANT: Gutman, George A.  
TITLE OF INVENTION: A No. 5559009el Voltage-Gated Potassium Channel  
TITLE OF INVENTION: Gene  
NUMBER OF SEQUENCES: 21  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: United States  
ZIP: 94111-4187

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/288,405A  
FILING DATE: 10-AUG-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/207,431  
FILING DATE: 04-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Dreser, Walter H.  
REGISTRATION NUMBER: A-59844-1/WHD  
REFERENCE/DOCKET NUMBER:

Qy 1 LXR 3  
Db 1 LTR 4

RESULT 4  
US-08-336-343A-36  
Sequence 36, Application US/08336343A  
GENERAL INFORMATION:  
PATENT NO. 5677144  
APPLICANT: Ullrich, Axel  
APPLICANT: Alves, Frauke  
TITLE OF INVENTION: CCK-2, A No. 5677144el Receptor Tyrosine Kinase  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/336,343A  
FILING DATE: 08-NOV-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7683-065  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 69-9747-8864  
TELEFAX: (212) 69-9747-8864  
TELEX: 65141 PENNIE  
INFORMATION FOR SEQ ID NO: 36:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-336-343A-36

Query Match: Score 9; DB 1; Length 4;  
Best Local Similarity 66.7%; Pred. No. 2.9e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LXR 3  
Db 2 LSR 4

RESULT 5  
US-09-142-078-19

Sequence 19, Application US/09142078  
; Patent No. 6,172,041  
; GENERAL INFORMATION:  
; APPLICANT: McCabe, R. Tyler  
; APPLICANT: Zhou, Li-Ming  
; APPLICANT: Layer, Richard T.  
; TITLE OF INVENTION: Use of Conantokins  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEES: Rochwell, Figg, Ernst & Kurz, P.C.  
; STREET: 555 Thirteenth Street, N.W., Suite 701-E  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy diskible  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/142,078  
; FILING DATE: 10-FEB-1999  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO US97/12652  
; FILING DATE: 21-JUL-1997  
; PRIOR APPLICATION DATA:  
; NAME: Ihnen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; REFERENCE/DOCKET NUMBER: 2314-135.A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-783-6040  
; TELEFAX: 202-783-6031  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRAINDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; FEATURES:  
; NAME/KEY: Modified site  
; LOCATION: 4  
; OTHER INFORMATION: /note= "Xaa is  
; gamma-carboxyglutamic acid"  
; US-09-142-078-19

Query Match 81.8%; Score 9; DB 3; Length 4;  
; Best Local Similarity 66.7%; Pred. No. 2.9e+05;  
; Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
Db 1 LAR 3

---

RESULT 6  
US-09-357-141-19  
; Sequence 19, Application US/09357141  
; Patent No. 6,277,825  
; GENERAL INFORMATION:  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; APPLICANT: McCabe, R. Tyler  
; APPLICANT: Layer, Richard T.  
; APPLICANT: Zhou, Li-Ming

; TITLE OF INVENTION: Use of Conantokins for Treating Pain  
; FILE REFERENCE: 2314-171  
; CURRENT APPLICATION NUMBER: US/09/357,141  
; PRIOR APPLICATION NUMBER: US 09/283,277  
; PRIOR FILING DATE: 1999-04-01  
; PRIOR APPLICATION NUMBER: US 09/142,078  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: WO US97/12652  
; PRIOR FILING DATE: 1997-07-21  
; PRIOR APPLICATION NUMBER: US 08/762,377  
; PRIOR FILING DATE: 1996-12-06  
; PRIOR APPLICATION NUMBER: US 08/684,750  
; PRIOR FILING DATE: 1996-07-22  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Conus radiatus  
; FEATURE:  
; NAME/KEY: PEPTIDE  
; LOCATION: (4)  
; OTHER INFORMATION: Xaa is gamma-carboxyglutamic acid.  
; US-09-357-141-19  
Query Match 81.8%; Score 9; DB 3; Length 4;  
; Best Local Similarity 66.7%; Pred. No. 2.9e+05;  
; Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
Db 1 LAR 3

---

RESULT 7  
US-09-533-889-19  
; Sequence 19, Application US/09353889  
; Patent No. 6,399,574  
; GENERAL INFORMATION:  
; APPLICANT: McCabe, R. Tyler  
; APPLICANT: Zhou, Li-Ming  
; APPLICANT: Layer, Richard T.  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: McIntosh, J. Michael  
; TITLE OF INVENTION: Use of Conantokins  
; NUMBER OF SEQUENCES: 71  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.  
; STREET: 555 Thirteenth Street, N.W., Suite 701-E  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZPL: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/533,889  
; FILING DATE: 22 MAR-2000  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 09/142,078  
; FILING DATE: 10-FEB-1999  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: WO US97/12652  
; FILING DATE: 21-JUL-1997  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/762,377  
; FILING DATE: 06-DEC-1996  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/684,750  
; APPLICATION NUMBER: US 09/684,750

FILING DATE: 22-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28, 957  
 REFERENCE/DOCKET NUMBER: 2314-168.A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-783-6040  
 TELEX/FAX: 202-783-6031  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <Unknown>  
 TOPOLogy: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 FEATURE: NAME/KEY: Modified-site  
 LOCATION: 4  
 OTHER INFORMATION: /note= "Xaa is gamma-carboxyglutamic acid"  
 US-09-333-889-19

Query Match Score 9; DB 4; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 1 LAR 3

RESULT 8  
 US-09-142-080-19  
 Sequence 19, Application US/09142080  
 Patent No. 6515103

GENERAL INFORMATION:  
 APPLICANT: Abogadie, Fe C.  
 Cruz, Lourdes J.  
 Olivera, Baldomero M.  
 Walker, Craig  
 Collidge, Clark  
 Hilliard, David R.  
 Jimenez, Elsie  
 Layer, Richard T.  
 Zhou, Li-Ming  
 McCabe, R. Tyler  
 TITLE OF INVENTION: Conantokins  
 NUMBER OF SEQUENCES: 71  
 CORRESPONDENCE ADDRESS:  
 STREET: 555 Thirteenth Street, N.W., Suite 701-E  
 CITY: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY disk  
 COMPUTER: IBM PC Compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/142.080  
 FILING DATE: 11-May-2000  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: WO US97/12618  
 FILING DATE: 21-JUL-1997  
 APPLICATION NUMBER: US 08/684,742  
 FILING DATE: 22-JUL-1996

ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28, 957  
 REFERENCE/DOCKET NUMBER: 2314-134.A

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-783-6040  
 TELEX/FAX: 202-783-6031  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <Unknown>  
 TOPOLogy: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 FEATURE: NAME/KEY: Modified-site  
 LOCATION: 4  
 OTHER INFORMATION: /note= "Xaa is gamma-carboxyglutamic acid"  
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
 US-09-142-080-19

Query Match Score 9; DB 4; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 1 LAR 3

RESULT 9  
 US-19-486-283C-4  
 Sequence 4, Application US/09486283C  
 Patent No. 6573243

GENERAL INFORMATION:  
 APPLICANT: ITAGAKI, Yasuhiro  
 APPLICANT: KONNO, Yasuhiro  
 APPLICANT: KAWAI, No. 657323ufumi  
 APPLICANT: TARAYANA, Hiroaki  
 TITLE OF INVENTION: POMPILID WASP-DERIVED NEUROPEPTIDES  
 FILE REFERENCE: 1830/48652  
 CURRENT FILING DATE: 2000-05-19  
 PRIORITY APPLICATION NUMBER: JP 9/241699  
 PRIORITY FILING DATE: 1997-08-25  
 PRIORITY APPLICATION NUMBER: PCT/JP98/03730  
 PRIORITY FILING DATE: 1998-08-24  
 NUMBER OF SEQ ID NOS: 203  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO 4

Query Match Score 9; DB 4; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 1 LAR 3

RESULT 10  
 US-09-335-852-355  
 Sequence 355, Application US/09535852

GENERAL INFORMATION:  
 PATENT NO. 6636911  
 APPLICANT: Blachuk, Orest W.  
 APPLICANT: Symonds, James W.  
 APPLICANT: Gour, Barbara J.  
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING DESMOSOMAL CADHERIN-MEDIATED FUNCTIONS  
 FILE REFERENCE: 100086.4076

CURRENT APPLICATION NUMBER: US/09/535,852  
 CURRENT FILING DATE: 2001-05-21  
 NUMBER OF SEQ ID NOS: 2009  
 SEQ ID NO: 355  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Unknown  
 OTHER INFORMATION: NO. 6638911 classical cadherin calcium binding motif  
 US-09-535-852-355

Query Match 81.8%; Score 9; DB 4; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 LXR 3  
 Db 1 LTR 3

RESULT 11  
 US-07-626-923A-12  
 Sequence 12, Application US/07626923A  
 GENERAL INFORMATION:  
 APPLICANT: Yoshimura, Akihiko  
 APPLICANT: Longmore, Gregory D.  
 APPLICANT: Lodish, Harvey  
 TITLE OF INVENTION: MUTANT EPO RECEPTOR AND USES  
 NUMBER OF SEQUENCES: 14  
 CURRENT APPLICATION NUMBER: #1.25  
 ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.  
 STREET: Two Militia Drive  
 CITY: Lexington  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02173  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/626-923A  
 FILING DATE: 13 December 1990  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Granahan, Patricia  
 REGISTRATION NUMBER: 32,227  
 REFERENCE/DOCKET NUMBER: WH190-08  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 861-6240  
 TELEFAX: (617) 861-9540  
 INFORMATION FOR SEQ ID NO: 12:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-07-626-923A-12

Query Match 81.8%; Score 9; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 LXR 3  
 Db 1 LAR 3

RESULT 12  
 US-08-357-264-5

Sequence 5, Application US/08357264  
 Patent No. 5541077  
 GENERAL INFORMATION:  
 APPLICANT: BURNIE Mr., James P.  
 APPLICANT: MATTHEWS Ms., Ruth C.  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cushman, Darby & Cushman  
 STREET: 1100 New York Avenue, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3918  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/357,264  
 FILING DATE: 10-JULY-1991  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/152669  
 FILING DATE: 16-NOV-1993  
 APPLICATION NUMBER: US 663897  
 FILING DATE: 14 MAR-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, Paul N.  
 REGISTRATION NUMBER:  
 REFERENCE/DOCKET NUMBER: PNK/5544/202253/DJP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-861-3000  
 TELEFAX: 202-822-0944  
 TELEX: 671467 CUSH  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-357-264-5

Query Match 81.8%; Score 9; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 1 LSR 3

RESULT 13  
 US-08-456-840-38  
 Sequence 38, Application US/08456840  
 Patent No. 5597908  
 GENERAL INFORMATION:  
 APPLICANT: Tadeei-Peters, W. C.  
 APPLICANT: Butler, Sandra M.  
 TITLE OF INVENTION: Immunoactive Peptides of Apo (a)  
 NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Akzo No. 5597908el  
 STREET: 1330 Piccard Drive  
 CITY: Rockville  
 STATE: Maryland  
 COUNTRY: US  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/455,840  
 FILING DATE: 01-JUN-1995  
 CLASSIFICATION: 536  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/266,407  
 FILING DATE: 27-JUN-1994  
 APPLICATION NUMBER: US 08/172,461  
 FILING DATE: 21-DEC-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Gormley, Mary E.  
 REGISTRATION NUMBER: 34,409  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 301-258-5200  
 TELEFAX: 301-977-0847  
 INFORMATION FOR SEQ ID NO: 38:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-455-840-38

RESULT 14  
 US-08-672-514-5  
 Sequence 5, Application US/08672514  
 Patent No. 5686248  
 GENERAL INFORMATION:  
 APPLICANT: BURNIE Mr., James P.  
 APPLICANT: MATTHEWS Ms., Ruth C.  
 TITLE OF INVENTION: FUNGAL STRESS PROTEINS  
 NUMBER OF SEQUENCES: 10  
 ADDRESSEE: Cushman, Darby & Cushman  
 STREET: 1100 New York Avenue, N.W.  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-3918  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/672,514  
 FILING DATE: 28-JUN-1996  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/152,669  
 FILING DATE: 16-NOV-1993  
 APPLICATION NUMBER: US 08/152669  
 FILING DATE: 16-NOV-1993  
 APPLICATION NUMBER: US 663897  
 FILING DATE: 14-MAR-1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KOKULIS, Paul N.  
 REGISTRATION NUMBER: 16773  
 REFERENCE/DOCKET NUMBER: PNK/5544/202253/DJJP  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-861-3000  
 TELEX: 6714627 CUSH

INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-672-514-5

Query Match 81.8%; Score 9; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 |  
 Db 1 LSR 3

RESULT 15  
 US-07-789-184-173  
 Sequence 173, Application US/07789184  
 Patent No. 5688768  
 GENERAL INFORMATION:  
 APPLICANT: COUGHLIN, SHAUN R.  
 APPLICANT: SCARBROUGH, ROBERT M.  
 TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND  
 TITLE OF INVENTION: RELATED PHARMACEUTICALS  
 NUMBER OF SEQUENCES: 223  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MORRISON & FOERSTER  
 STREET: 755 Page Mill Road  
 CITY: Palo Alto  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94304-1018  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/789,184  
 FILING DATE: 1991107  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MURASHIGE, KATE H.  
 REGISTRATION NUMBER: 29,959  
 REFERENCE/DOCKET NUMBER: 220000-20502.20  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 813-5600  
 TELEFAX: (415) 494-0792  
 TELEX: 34-0154  
 INFORMATION FOR SEQ ID NO: 173:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5 amino acids  
 TYPE: AMINO ACID  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 5  
 OTHER INFORMATION: /note= "This position is R-NH2."  
 US-07-789-184-173

Query Match 81.8%; Score 9; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 |  
 Db 3 LAR 5



This Page Blank (uspto)

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 07:35:06 ; Search time 34:4421 Seconds

(without alignments)  
37.345 Million cell updates/sec

Title: US-09-498-556C-357

Perfect score: 11

Sequence: 1 LXRX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 100%  
Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	9	81.8	Sequence 2, Appli	4 9 US-09-248-158-2
2	9	81.8	Sequence 8, Appli	4 9 US-09-838-652a-8
3	9	81.8	Sequence 5, Appli	4 10 US-09-552-910-5
4	9	81.8	Sequence 155, App	4 10 US-09-552-910-155
5	9	81.8	Sequence 6, Appli	4 12 US-09-349-924-6
6	9	81.8	Sequence 674, App	4 12 US-09-335-410-674
7	9	81.8	Sequence 33, Appli	4 12 US-10-261-161-33
8	9	81.8	Sequence 295, App	4 14 US-10-306-639-295
9	9	81.8	Sequence 6, Appli	4 14 US-10-028-075B-6
10	9	81.8	Sequence 6, Appli	4 14 US-10-029-206A-6
11	9	81.8	Sequence 6, Appli	4 14 US-10-44-709-6
12	9	81.8	Sequence 19, Appli	4 14 US-10-357-467-19
13	9	81.8	Sequence 674, App	4 14 US-10-277-222-674
14	9	81.8	Sequence 674, App	4 15 US-10-38-390-674
15	9	81.8	Sequence 115, App	4 15 US-10-391-399-115

#### ALIGNMENTS

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RESULT 1
US-09-248-158-2
; Sequence 2, Application US/09248158
; Patent No. US20020015678A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Zhong-Xiao
; TITLE OF INVENTION: Direct Adsorption Scintillation Assay
; FOR Measuring Enzyme Activity and Assaying Biochemical
; TITLE OF INVENTION: Processes
; FILE REFERENCE: 342312000600
; CURRENT APPLICATION NUMBER: US/09/248-158
; PRIORITY FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/074,272
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-09-248-158-2
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RESULT 2
US-09-818-656A-8
; Sequence 8, Application US/09818656A1
; Patent No. US20020142381A1
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/ GENERAL INFORMATION:
/   APPLICANT: GONG, Fangcheng et al.
/   TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
/   TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
/   TITLE OF INVENTION: AND USES THEREOF
/   FILE REFERENCE: C10-01191
/   CURRENT APPLICATION NUMBER: US/09/818,656A
/   CURRENT FILING DATE: 2000-03-28
/   NUMBER OF SEQ ID NOS: 103
/   SOFTWARE: FastSEQ for Windows Version 4.0
/   SEQ ID NO: 8
/   LENGTH: 8
/   TYPE: PRT
/   ORGANISM: Homo sapiens
/   US-09-818-656A-8

Query Match          81.8%; Score 9; DB 9; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LXR 3
       | 
       2 LTR 4

RESULT 3
US-09-852-910-5
Sequence 5, Application US/09852910
Publication No. US20030096297A1
GENERAL INFORMATION:
APPLICANT: Hamm, Heidi
TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptors
FILE REFERENCE: 2661-101
CURRENT APPLICATION NUMBER: US/09/852,910
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US 60/275,472
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 271
SOFTWARE: Patentin version 3.0
SEQ ID NO: 5
LENGTH: 4
TYPE: PRT
ORGANISM: mammal
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)-(4)
OTHER INFORMATION: PAR-23
US-09-852-910-5

Query Match          81.8%; Score 9; DB 10; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 LXR 3
       | 
       1 LSR 3

RESULT 4
US 09-852-910-155
Sequence 155, Application US/09852910
Publication No. US20030096297A1
GENERAL INFORMATION:
APPLICANT: Hamm, Heidi
TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptors
FILE REFERENCE: 2661-101
CURRENT APPLICATION NUMBER: US/09/852,910
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US 60/275,472
PRIOR FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 271

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; CURRENT FILING DATE: 2001-08-22 ; PRIOR APPLICATION NUMBER: US 60/351,289
; PRIOR FILING DATE: 2001-10-29 ; PRIOR APPLICATION NUMBER: US 60/366,854
; PRIOR FILING DATE: 2000-08-22 ; PRIOR APPLICATION NUMBER: US 60/282,739
; PRIOR FILING DATE: 2001-04-10 ; PRIOR APPLICATION NUMBER: US 60/385,362
; NUMBER OF SEQ ID NOS: 700 ; PRIOR FILING DATE: 2002-06-03
; SOFTWARE: PatentIn Ver. 2.1 ; NUMBER OF SEQ ID NOS: 307
; SEQ ID NO: 674 ; SOFTWARE: PatentIn version 3.1
; LENGTH: 4 ; SEQ ID NO: 295
; TYPE: PRT ; LENGTH: 4
; ORGANISM: Artificial Sequence ; TYPE: PRT
; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif
US-09-498-556c-357.sep04.rapb ; ORGANISM: Homo sapiens
; OTHER INFORMATION: ; US-10-206-699-295

Query Match Score 9; DB 12; Length 4;
Best Local Similarity 61.8%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LXR 3
Db 2 LTR 4

RESULT 7
US-10-261-161-33
; Sequence 33, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Silas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO: 33
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: swiss/P36507/MPK2 Human
; OTHER INFORMATION: ; US-10-028-075B-6

Query Match Score 9; DB 14; Length 4;
Best Local Similarity 61.8%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LXR 3
Db 2 LTR 4

RESULT 8
US-10-206-699-295
; Sequence 295, Application US/10206699
; Publication No. US20030100510A1
; GENERAL INFORMATION:
; APPLICANT: Sundararaoorthy, M.
; TITLE OF INVENTION: Crystallized structure of Type IV Collagen NCI Domain Hexamer
; FILE REFERENCE: MBBB 01-1017
; CURRENT APPLICATION NUMBER: US/10/206,699
; CURRENT FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 4
; TYPE: PRT
; OTHER INFORMATION: ; US-10-206-699-295

Query Match Score 9; DB 12; Length 4;
Best Local Similarity 61.8%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LXR 3
Db 2 LAR 4

RESULT 9
US-10-028-075B-6
; Sequence 6, Application US/10028075B
; Publication No. US20030113733A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Bennet, Robert
; TITLE OF INVENTION: Gene regulator
; FILE REFERENCE: 21B3-5220US
; CURRENT APPLICATION NUMBER: US/10/028,075B
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 175
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: swiss/P36507/MPK2 Human
; OTHER INFORMATION: ; US-10-028-075B-6

Query Match Score 9; DB 14; Length 4;
Best Local Similarity 61.8%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LXR 3
Db 2 LAR 4

RESULT 10
US-10-028-206A-6
; Sequence 6, Application US/10029206A
; Publication No. US2003011920A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Nisar A.
; APPLICANT: Bennet, Robert
; TITLE OF INVENTION: Oligopeptide treatment of anthrax
; FILE REFERENCE: 21B3-5220US
; CURRENT APPLICATION NUMBER: US/10/029,206A
; CURRENT FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 097821,380
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 6
; LENGTH: 4
; TYPE: PRT
; OTHER INFORMATION: ; US-10-028-206A-6

Query Match Score 9; DB 12; Length 4;
Best Local Similarity 61.8%; Pred. No. 1.2e+06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 LXR 3
Db 2 LAR 4

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ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Description of Artificial Sequence: peptide  
 US-10-029-206A-6

Query Match Score 9; DB 14; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 2 LAR 4

RESULT 11  
 US-10-244-709-6  
 ; Sequence 6, Application US/10244709  
 ; Publication No. US2003012976A1  
 GENERAL INFORMATION:  
 ; APPLICANT: FRED E. REGNIER  
 ; TITLE OF INVENTION: AFFINITY SELECTED SIGNATURE PEPTIDES FOR PROTEIN IDENTIFICATION A  
 ; TITLE OF INVENTION: QUANTIFICATION  
 ; FILE REFERENCE: 290..0001 0103  
 ; CURRENT APPLICATION NUMBER: US/10/244..709  
 ; CURRENT FILING DATE: 2002-09-16  
 ; PRIOR APPLICATION NUMBER: 60/0203..227  
 ; PRIOR FILING DATE: 2000-05-05  
 ; PRIOR APPLICATION NUMBER: 60/2008..184  
 ; PRIOR FILING DATE: 2000-05-31  
 ; PRIOR APPLICATION NUMBER: 60/2008..372  
 ; PRIOR FILING DATE: 2000-05-31  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO: 4  
 LENGTH: 4  
 TYPE: PRT  
 ORGANISM: Artificial  
 FEATURE:  
 OTHER INFORMATION: C-terminal sequence  
 US-10-244-709-6

Query Match Score 9; DB 14; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 2 LAR 4

RESULT 12  
 US-10-357-467-19  
 ; Sequence 19, Application US/10357467  
 ; Publication No. US2003019472A1  
 GENERAL INFORMATION:  
 ; APPLICANT: Abogadie, Fe C.  
 ; Cruz, Lourdes J.  
 ; Olivera, Baldomero M.  
 ; Walker, Craig  
 ; Colledge, Clark  
 ; Hilliard, David R.  
 ; Jimenez, Elsie  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSE: Rothwell, Figg, Ernst & Manbeck, p.c.  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/10/357,467  
 FILING DATE: 04-Feb-2003  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 09/142,080  
 FILING DATE: 15-MAY-2000  
 APPLICATION NUMBER: WO US97/12618  
 FILING DATE: 21-JUL-1997  
 APPLICATION NUMBER: US 08/684,742  
 FILING DATE: 22-JUL-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Innen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 2314-256.A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-783-6040  
 TELEFAX: 202-783-6031  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: <unknown>  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 FRAGMENT TYPE: internal  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 4  
 OTHER INFORMATION: /note= "Xaa is  
 gamma-carboxyglutamic acid"  
 SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
 US-10-357-467-19

Query Match Score 9; DB 14; Length 4;  
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 2 LAR 4

RESULT 13  
 US-10-277-292-674  
 ; Sequence 674, Application US/10277292  
 ; Publication No. US2003019947A1  
 GENERAL INFORMATION:  
 ; APPLICANT: FARIS, MARY  
 ; APPLICANT: HUBERT, RENE  
 ; APPLICANT: RAITANO, ARTHUR  
 ; APPLICANT: AFAR, DANIEL  
 ; APPLICANT: LEVIN, ELANA  
 ; APPLICANT: CRALLIA-BED, PAOLA  
 ; APPLICANT: JAROBOVITZ, AYA  
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7  
 ; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 ; TITLE OF INVENTION: OTHER CANCERS  
 ; FILE REFERENCE: 51158-20050.00  
 ; CURRENT APPLICATION NUMBER: US/10/277,292  
 ; CURRENT FILING DATE: 2002-10-21  
 ; PRIOR APPLICATION NUMBER: US/09/935,430  
 ; PRIOR FILING DATE: 2001-08-22  
 ; PRIOR APPLICATION NUMBER: 60/227,098  
 ; PRIOR FILING DATE: 2000-08-22  
 ; PRIOR APPLICATION NUMBER: 60/282,739  
 ; PRIOR FILING DATE: 2001-04-10  
 ; NUMBER OF SEQ ID NOS: 700  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO: 674  
 LENGTH: 4

; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE: Description of Artificial Sequence: Peptide motif  
 ; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
 US-10-277-292-674  
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 Matches 2;    Conservative 0;    Mismatches 1;    Indels 0;    Gaps 0;  
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 Db                1 |  
 Db                2 LTR 4

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RESULT 14  
 US-10-280-340-674  
 ; Sequence 674, Application US/10280340  
 ; Publication No. US20030207835A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: FARIS, MARY  
 ; APPLICANT: HUBERT, RENE  
 ; APPLICANT: RAITANO, ARTHUR  
 ; APPLICANT: AFAR, DANIEL  
 ; APPLICANT: LEVIN, ELANA  
 ; APPLICANT: CHALLITA-EID, PIA  
 ; APPLICANT: JAKOBOWITZ, AYA  
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158PPD7  
 ; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND  
 ; TITLE OF INVENTION: OTHER CANCERS  
 ; CURRENT APPLICATION NUMBER: US/10/280,340  
 ; CURRENT FILING DATE: 2002-10-25  
 ; PRIOR APPLICATION NUMBER: US/09/935,430  
 ; PRIOR FILING DATE: 2001-08-22  
 ; PRIOR APPLICATION NUMBER: 60/227,098  
 ; PRIOR FILING DATE: 2000-08-22  
 ; PRIOR APPLICATION NUMBER: 60/282,739  
 ; PRIOR FILING DATE: 2001-04-10  
 ; NUMBER OF SEQ ID NOS: 700  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO: 674  
 ; LENGTH: 4

; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE: Description of Artificial Sequence: Peptide motif  
 ; OTHER INFORMATION: Description of Artificial Sequence: Peptide motif  
 US-10-280-340-674

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Query Match      81.8%;    Score 9;    DB 15;    Length 4;  
 Best Local Similarity 66.7%;    Pred. No. 1.2e+06;  
 Matches 2;    Conservative 0;    Mismatches 1;    Indels 0;    Gaps 0;  
 Qy                1 LXR 3  
 Db                1 |  
 Db                2 LTR 4

Search completed: September 24, 2004, 08:10:04  
Job time : 34.4421 secs

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RESULT 15  
 US-10-391-399-115  
 ; Sequence 115, Application US/10391399  
 ; Publication No. US20030219806A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Millennium Pharmaceuticals, Inc.  
 ; APPLICANT: Gluckmann, Maria Alexandra  
 ; APPLICANT: Curtis, Rory A. J.  
 ; APPLICANT: Lora, Jose M.  
 ; APPLICANT: Galvin, Katherine M.  
 ; APPLICANT: Silos-Santiago, Inmaculada  
 ; TITLE OF INVENTION: NOVEL 18607, 15603, 69318, 12303, 48000,  
 ; TITLE OF INVENTION: 52920, 5433, 3854, 57301, 5824, 55063,  
 ; TITLE OF INVENTION: AND 33751 MOLECULES AND USES THEREFOR  
 ; FILE REFERENCE: MP103-000NM

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## OM protein - protein search, using sw model

Run on: September 24, 2004, 07:28:33 (without alignments)

157.555 Million cell updates/sec

Title: US-09-498-556C-357

Perfect score: 11

Sequence: 1 LXRX 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:

283366

Minimum DB seq length: 0  
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR-78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	9	81.8	7	B48394	major fat-globule
3	9	81.8	8	PC131	hypothetical prote
4	9	81.8	8	T13818	cytochrome oxidase
5	9	81.8	10	T13838	cytochrome-c oxidase
6	9	81.8	10	T1219	dextrantraserase (EC
7	9	81.8	11	PU0034	cytochrome P450D27
8	9	81.8	12	A42324	Ig heavy chain CRD
9	9	81.8	13	PT0293	protein QAI00054 -
10	9	81.8	14	PA0111	ribosomal protein
11	9	81.8	15	S38896	fructose-bisphosph
12	9	81.8	15	PA0075	hypothetical prote
13	9	81.8	15	PA0102	T-cell receptor al
14	9	81.8	15	B32800	phe leader peptide
15	9	81.8	15	PH1455	insulin-like growth
16	9	81.8	15	AF0432	chymotrypsin (EC 3
17	9	81.8	16	JH0517	collagen alpha 1(X
18	9	81.8	16	C61414	ribosomal protein
19	9	81.8	16	B44036	ribosomal protein
20	9	81.8	17	JP0046	vitamin D binding
21	9	81.8	17	A34835	hypothetical 2.1K
22	9	81.8	17	I54269	chymotrypsin (EC 3
23	9	81.8	17	JQ3310	GTP-binding protein
24	9	81.8	17	JQ2320	IcrKC - Yersinia p
25	9	81.8	17	B61414	orf15' of aadR -
26	9	81.8	18	S29491	hypothetical prote
27	9	81.8	18	A41877	
28	9	81.8	18	A43334	
29	9	81.8	18	S33645	

## ALIGNMENTS

RESULT 1						
E48394	Glycoprotein component 16/major fat-globule membrane protein/MFG-E8 homolog - bovine (Fr)					
C;Species: Bos primigenius taurus (cattle)						
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997						
C;Accession: E48394						
R;Mather, I.H.; Baughart, L.R.; Lane, W.S.						
Biochem. Mol. Biol. Int. 29, 545-554, 1993						
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.						
A;Reference number: A48394; PMID:93250576; PMID:8485470						
A;Accession: E48394						
C;Keywords: glycoprotein						
A;Molecule type: Protein						
A;Residues: 1-7 <XMT>						
A;Experimental source: milk						
A;Note: sequence extracted from NCBI backbone (NCBIP:131450)						
Query Match	B1.8%;	Score 9;	DB 2;	Length 7;		
Matches	2;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1 LXR 3					
Db	5 LAR 7					
RESULT 2						
B48394	major fat-globule membrane protein GP 55 - guinea pig (fragment)					
C;Species: Cavia porcellus (Guinea pig)						
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995						
C;Accession: B48394						
R;Mather, I.H.; Baughart, L.R.; Lane, W.S.						
Biochem. Mol. Biol. Int. 29, 545-554, 1993						
A;Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig II-like sequences.						
A;Reference number: A48394; PMID:93250576; PMID:8485470						
A;Accession: B48394						
C;Keywords: preliminary						
A;Molecule type: protein						
A;Residues: 1-7 <XMT>						
A;Experimental source: milk						
A;Note: sequence extracted from NCBI backbone (NCBIP:131444)						
Query Match	B1.8%;	Score 9;	DB 2;	Length 7;		
Matches	2;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	1 LXR 3					

Db 5 LXR 7

RESULT 3  
 PC4131 hypothetical protein 8 [imported] - *Pseudomonas aeruginosa* (fragment)  
 C;Species: *Pseudomonas aeruginosa*  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C;Accession: PC4131  
 R;Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.  
 Gene 167, 87-91, 1995  
 A;Title: Sequencing and characterization of the downstream region of the genes encoding  
 Y for biosynthesis of heme d1.  
 A;Reference number: JC4552; MUID: 96144254; PMID: 8566817  
 A;Accession: PC4131  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-8 <KAW>  
 A;Cross-references: DDBJ:D50473; NID:g1217594  
 A;Note: this ORF is not annotated in GenBank entry PSENIRC, release 113.0  
 Query Match 81.8%; Score 9; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 A;Title: Two novel gene orders and the role of light-strand replication in rearrangement  
 A;Reference number: Z17789; MUID: 97153826; PMID: 9000757  
 A;Accession: T14219  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-10 <MAC>

A;Cross-references: EMBL:U71333; NID:g1753232; PID:91753235; PIDN:AAB48271.1  
 C;Genetics:  
 A;Genome: COI  
 C;Keywords: mitochondrion; oxidoreductase

Query Match 81.8%; Score 9; DB 2; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 3 LTR 5

RESULT 6  
 T14219 cytochrome-c oxidase (EC 1.9.3.1) chain I - *Xenosaurus grandis* mitochondrion (fragment)  
 C;Species: mitochondrion *Xenosaurus grandis*  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
 C;Accession: T14219  
 R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.  
 Mol. Biol. Evol. 14, 91-104, 1997  
 A;Title: Two novel gene orders and the role of light-strand replication in rearrangement  
 A;Reference number: Z17789; MUID: 97153826; PMID: 9000757  
 A;Accession: T14219  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-10 <MAC>

A;Cross-references: EMBL:U71333; NID:g1753236; PIDN: AAC62821.1; PID:91753275  
 C;Genetics:  
 A;Genome: COI  
 C;Keywords: mitochondrion; oxidoreductase

Query Match 81.8%; Score 9; DB 2; Length 10;  
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 3 LTR 5

RESULT 4  
 T13818 cytochrome oxidase subunit I - Atlantic halibut mitochondrial (fragment)  
 C;Species: mitochondrial Myxine glutinosa (Atlantic halibut)  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 21-Jul-2000  
 C;Accession: T13818  
 R;Delarre, C.; Barriell, V.; Tillier, S.; Janvier, P.; Gachelin, G.  
 Mol. Biol. Evol. 14, 807-813, 1997  
 A;Title: The main features of the craniate mitochondrial DNA between the ND1 and the COI  
 A;Reference number: Z17775; MUID: 97398704;  
 A;Accession: T13818  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-8 <DEL>  
 A;Cross-references: EMBL:Y09527; NID:g2340019; PIDN:CAA70718.1; PID:92340022  
 C;Genetics:  
 A;Genome: mitochondrion  
 A;Note: COI  
 C;Keywords: mitochondrion

Query Match 81.8%; Score 9; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 3 LSR 5

RESULT 5  
 T13838 cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipus biporus mitochondrion (fragment)  
 C;Species: mitochondrion Bipus biporus  
 C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 11-May-2000  
 C;Accession: T13838  
 R;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Fang, Z.; Papenfuss, T.J.  
 Mol. Biol. Evol. 14, 91-104, 1997  
 A;Title: Two novel gene orders and the role of light-strand replication in rearrangement  
 A;Reference number: Z17789; MUID: 97153826; PMID: 9000757  
 A;Accession: T13838  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-10 <MAC>

Query Match 81.8%; Score 9; DB 2; Length 11;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 8 LTR 10

RESULT 8  
 A4224 cytochrome P450C27/25 - rat (fragment)  
 C;Species: *Rattus norvegicus* (Norway rat)



Db 6 LSR 8

RESULT 14  
 B32800 hypothetical protein (P1 5' region) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Accession: B32800  
 C;Date: 22-Nov-1989 #sequence\_revision 22-Nov-1989 #text\_change 30-Sep-1993  
 R;Jindal, S.; Duddani, A.K.; Singh, B.; Harley, C.B.; Gupta, R.S.  
*Mol. Cell. Biol.* 9, 279-283, 1989  
 A;Title: Primary structure of a human mitochondrial protein homologous to the bacterial  
 A;Reference number: A32800; MUID:89313783; PMID:2568584  
 A;Accession: B32800  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-15 <JIN>  
 A;Cross-references: GB:M22382

Query Match Similarity 81.8%; Score 9; DB 2; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 LXR 3  
       |  
       3 LSR 5  
 Db

RESULT 15  
 PH1455 T-cell receptor alpha chain (clone A24/PER4) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 11-Apr-1995  
 C;Accession: PH1455  
 R;Casanova, J.L.; Marinoni, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ro  
*J. Exp. Med.* 177, 811-820, 1993  
 A;Title: T cell receptor selection by and recognition of two class I major histocompatib  
 A;Reference number: PH1430; MUID:93171821; PMID:8436911  
 A;Accession: PH1455  
 A;Molecule type: mRNA  
 A;Residues: 1-15 <CAS>  
 A;Experimental source: cytolytic T-lymphocyte  
 C;Superfamily: immunoglobulin homology  
 C;Keywords: receptor; T-cell

Query Match Similarity 81.8%; Score 9; DB 2; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 LXR 3  
       |  
       3 LSR 5  
 Db

Search completed: September 24, 2004, 07:36:05  
 Job time : 5.44211 secs

BLOSUM62 Scoring table: Gapop 10.0 , Gapext 0.5						
Database : SwissProt_42:*						
Run on: September 24, 2004, 07:28:33 ; Search time 1.38947 Seconds (without alignments) 149.899 Million cell updates/sec						
Title: US-09-498-556C-357						
Perfect score: 11						
Sequence: 1 LXRX 4						
Scoring table:						
Post-processing: Minimum Match 0% Maximum Match 100%						
Listing first 45 summaries						
Total number of hits satisfying chosen parameters: 141681						
Minimum DB seq. length: 0 Maximum DB seq. length: 2000000000						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query	Match	Length	DB	ID
1	9	81.8	11	1	B310_ONCNY	P83328_oncorhynchus
2	9	81.8	15	1	ONC1_ONCNY	P80287_oncorhynchus
3	9	81.8	15	1	UC25_MAIZE	P80631_zea_mays_(
4	9	81.8	16	1	IB44_PIG	P24854_sus_scrofa
5	9	81.8	18	1	YAH5_RHOPA	P02005_rhodopsin
6	9	81.8	20	1	LYC_FELCA	P37155_azetobacte
7	9	81.8	20	1	RECX_AZOTI	P37863_azotobacter
8	9	81.8	21	1	SVA RAT	P50475_ratius_nor
9	9	81.8	22	1	ANFC_CHICK	P21805_gallus_gal
10	9	81.8	23	1	GNA_PHLGP	P20479_phormidium
11	9	81.8	25	1	IPLR_PSEAN	P80898_pseudanaba
12	9	81.8	25	1	NEUO_RANTE	P20056_rana_tempo
13	9	81.8	25	1	SPIG_PSEAGT	P23357_pseudacanth
14	9	81.8	25	1	UBL1_BOVIN	P23356_bos_taurus
15	9	81.8	26	1	NTRC_RHILP	P41502_rhizobium
16	9	81.8	26	1	YFFA_KLEBOX	P21710_klebsiella
17	9	81.8	27	1	CXER_CONRA	P58806_conus_radi
18	9	81.8	27	1	SECR_CANFA	P09910_canis_fami
19	9	81.8	27	1	SECR_RABIT	P32647_oryctolagus
20	9	81.8	27	1	SECR_SHEEP	P31299_ovis_aries
21	9	81.8	28	1	VIO_VACCP	P00334_vaccinia_v
22	9	81.8	29	1	HS98_NEUFR	P31540_neurospora
23	9	81.8	29	1	Y51_BPT3	P20326_bacterioph
24	9	81.8	31	1	A98A_DROMB	P046201_drosophila
25	9	81.8	31	1	DIND_DIPDU	P81710_diplopoda
26	9	81.8	33	1	LYC2_HORSE	P81710_equus_caba
27	9	81.8	33	1	OTCC_PSEPU	P11727_pseudomonas
28	9	81.8	33	1	PK1_DICDI	P3401_dicytostelium
29	9	81.8	34	1	RNL1_PIG	P15466_sus_scrofa
30	9	81.8	36	1	F4RE_METOC	P80951_mechanogen
31	9	81.8	36	1	PAHO_CERSI	P37999_ceratotheri
32	9	81.8	36	1	PAHO_CHTER	P41519_chinchilla
33	9	81.8	36	1	PAHO_DIDMA	P18107_didelphis

34	9	81.8	3.6	1	PAHO_EQUIZ	P38000 equus zebra
35	9	81.8	3.6	1	PAHO_ERIEU	P41335 erinaceus e
36	9	81.8	3.6	1	PAHO_MACMU	P33684 macaca mulatta
37	9	81.8	3.6	1	PAHO_RABIT	P41336 oryctolagus cuniculus
38	9	81.8	3.6	1	PAHO_TAPPI	P39559 tapirus pin
39	9	81.8	3.6	1	PYY_ANICA	P29305 amia calva
40	9	81.8	3.6	1	PYY_PIG	P01305 sus scrofa
41	9	81.8	3.6	1	YHDS_BACSU	P07588 bacillus su
42	9	81.8	3.7	1	CALI_PIG	P30580 sus scrofa
43	9	81.8	3.7	1	CALI_SHEEP	P30581 ovis aries
44	9	81.8	3.7	1	CALR_RANRI	P31688 rana ridibunda
45	9	81.8	3.7	1	PIP7_BOVIN	P21671 bos taurus
ALIGNMENTS						
RESULT 1						
ID	RS30_ONCNY	STANDARD;	PRT;	11 AA.		
AC	PR3328;					
DT	28-FEB-2003	(Rel. 41, Created)				
DT	28-FEB-2003	Last sequence update				
DT	10-OCT-2003	(Rel. 42, Last annotation update)				
DE	40S ribosomal protein S30 (Fragment).					
GN	PAU.					
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).					
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostei;					
OC	Actinopterygii; Neopeltidi; Teleostei; Euteleosteoi;					
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.					
OC	NCBI_TAXID=1022;					
OX	[1]					
RN	SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.					
RP	TISSUE-Skin mucous					
RC						
RC	MEDLINE-22142142; PubMed-12147245;					
RA	Fernandes J.M.O.; Smith V.J.;					
RT	"A novel antimicrobial function for a ribosomal peptide from rainbow trout skin."					
RL	Biochem. Biophys. Res. Commun. 296:1167-1171 (2002).					
CC	-!- FUNCTION: Has antibacterial activity against Gram-positive bacteria.					
CC	-!- MASS SPECTROMETRY: MW=6676.6 ; METHOD=MALDI.					
CC	-!- SIMILARITY: Belongs to the S30E family of ribosomal proteins.					
KW	Ribosomal Protein; Antibiotic.					
FT	NON-TER	11	11	MW;	2312AB630DD735B8 CRC64;	
SQ	SEQUENCE	11 AA;	1123			
Query Match		81.8%		Score 9;	DB 1;	Length 11;
Best Local Similarity		66.7%		Pred. No. 4e+02;		
Matches	2;	Conservative	0;	Mismatches	1;	Gaps 0
Qy	1 LXR 3					
Db	6 LAR 8					
RESULT 2						
ID	ONCL_ONCNY	STANDARD;	PRT;	15 AA.		
AC	PR8267;					
DT	28-FEB-2003	(Rel. 41, Created)				
DT	28-FEB-2003	Last sequence update				
DE	Oncorhynchus tshawytscha (Fragment).					
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).					
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostei;					
OC	Actinopterygii; Neopeltidi; Teleostei; Euteleosteoi;					
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.					
OX	NCBI_TAXID=8022;					
RP	SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.					
RP	TISSUE=skin mucous;					
RP	Medline-2034650; PubMed-10938737;					

RA Smith V.J., Fernandes J.M.O., Jones S.J., Kemp G.D., Tatner M.F.;  
 RT "Antibacterial Proteins in rainbow trout, Oncorhynchus mykiss.";  
 RL Fish Shallow ImmunoL 10:243-260 (2000).  
 CC -!- FUNCTION: Has antibacterial activity against Gram-positive  
 bacteria P. citreus.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Skin.  
 DR GO: GO:0005756; C: extracellular; NAS.  
 DR GO: GO:0003755; F: antimicrobial peptide activity; NAS.  
 DR GO: GO:0006805; P: xenobiotic metabolism; NAS.  
 KW Antibiotic.

UNSURE 4 OR G.  
 FT UNSURE 9 OR T.  
 NON-TER 15 15  
 SQ SEQUENCE 15 AA; 1601 MW; 43C25028DBC12B7C CRC64;

Query Match Score 9; DB 1; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 5.7e+02;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 12 LAR 14

RESULT 3  
 UC25\_MAIZE ID STANDARD; PRT; 15 AA.  
 AC P80631;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-DEC-1996 (Rel. 34, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Unknown Protein from 2D-page of etiolated coleoptile (Spot 77)  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD Clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE.

RC TISSUE=Coleoptile;  
 RC Prouzet P., Riccardi P., Morin C., Damerval C., Huet J. C.,  
 RA Pernot J.-C., Zivy M., de Vienne D.;  
 RT "The maize two dimensional gel protein database: towards an integrated  
 genome analysis program";  
 RT Theor. Appl. Gent. 93:997-1005 (1996).  
 CC -!- MICR��ELIANOUS: On the 2D-gel the determined PI of this unknown  
 CC protein is: 4.9, its MW is: 31.6 kDa.  
 DR Maize-DDPAGE; P80631; COLEOPTILE.  
 NON-TER 1 1  
 SQ SEQUENCE 15 AA; 1580 MW; 83C54CF0CE1614D0 CRC64;

Query Match Score 9; DB 1; Length 15;  
 Best Local Similarity 66.7%; Pred. No. 5.7e+02;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 5 LSR 7

RESULT 4  
 IBP4\_PIG ID STANDARD; PRT; 16 AA.  
 AC P24854;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Insulin-like growth factor-binding protein 4 (IGFBP-4) (IBP-4)  
 DE (IGF-binding protein 4) (Fragment).

GN IGFBP4.  
 OS Sus scrofa (Pig).  
 OC  
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Cetartiodactyla; Suina; Suidae; Sus  
 OX NCBITaxID=9823;  
 RN [1]  
 RP SEQUENCE.  
 MEDLINE=2109718; PubMed=1722398;  
 RX  
 RA Coleman M.B., Pan Y.-C.E., Etherton T.D.;  
 RT "Identification and NH2-terminal amino acid sequence of three  
 insulin-like growth factor-binding proteins in porcine serum.";  
 RL Biochem. Biophys. Res. Commun. 181:1131-1136 (1991).  
 CC -!- FUNCTION: IGF-binding proteins prolong the half-life of the IGFs  
 and have been shown to either inhibit or stimulate the growth  
 promoting effects of the IGFs on cell culture. They alter the  
 interaction of IGFs with their cell surface receptors.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Contains 1 IGFBP domain.  
 CC -!- SIMILARITY: Contains 1 thyroglobulin type-I domain.  
 DR PIR; JH0517; JH0517.  
 DR InterPro; IPR000867; Insl\_gro\_fac\_pr.  
 DR InterPro; IPR000716; Thyroglobulin\_1.  
 DR PROSITE; PS00222; IGF BINDING, PARTIAL.  
 DR PROSITE; PS00484; THYROGLOBULIN\_1; PARTIAL.  
 KW Growth factor binding.  
 NON-TER 16 16  
 SQ SEQUENCE 16 AA; 1799 MW; 40988810096655E2 CRC64;  
 Query Match Score 9; DB 1; Length 16;  
 Best Local Similarity 66.7%; Pred. No. 6.1e+02;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 14 LAR 16

RESULT 5  
 YAAS\_RHOFA ID STANDARD; PRT; 18 AA.  
 AC Q02055;  
 AC Q02055; RHOFA  
 AC Q02055; RHOPA  
 AC Q02055; RHOPA  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein in acrS region (Fragment).  
 OS Rhopseudomonas palustris.  
 OC Bacteria; Proteobacteria; Alpha-proteobacteria; Rhizobiales;  
 OC Bradyrhizobiaceae; Rhopseudomonas.  
 OX NCBI\_TaxID=1076;  
 RN [1]  
 RP SEQUENCE FROM N\_A.  
 RC STRAIN=GA009;  
 RX MEDLINE=92394882; PubMed=1522059;  
 RA Dispensa M., Thomas C.T., Kim M.K., Perrotta J.A., Gibson J., Harwood C.S.;  
 RT "Anaerobic growth of Rhopseudomonas palustris on 4-hydroxybenzoate  
 is dependent on AcrS, a member of the cyclic AMP receptor protein  
 family of transcriptional regulators.";  
 RT J. Bacteriol. 174:5803-5813 (1992).  
 RL  
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 CC  
 DR EMBL: M92426; AR26089.1;  
 DR PIR; A43334; A43334.  
 KW Hypothetical protein.  
 NON-TER 1  
 SQ SEQUENCE 18 AA; 2173 MW; 61DABDDE4E317B0A CRC64;

Query Match 81.8%; Score 9; DB 1; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 6.9e+02;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 1 LXR 3  
 Db 6 LTR 8

**RESULT 6**

LYC_FELICA	STANDARD;	PRT;	20 AA.
ID	LYC_FELICA		
AC	P37155;		
DT	01-OCT-1994 (Rel. 30, Created)		
DT	01-OCT-1994 (Rel. 30, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DB	Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylumuridase C) (Fragment), GN LYZ.		
OS	Felis silvestris catus (Cat).		
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.		
OX	NCBI_TaxID=9685;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE=Milk;		
RX	Medline=90263403; PubMed=2344734;		
RA	Halliday J.A., Bell K., McKenzie H.A., Shaw D.C.,		
RT	"Feline whey proteins: identification, isolation and initial characterization of alpha-lactalbumin, beta-lactoglobulin and lysozyme".		
RL	Comp. Biochem. Physiol. 95B:773-779(1990).		
CC	-!- FUNCTION: Lysozymes have primarily a bacteriolytic function; those in tissues and body fluids are associated with the monocyte-macrophage system and enhance the activity of immunoenzymes.		
CC	-!- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-acetyl-D-glucosamine and N-acetylumuramic acid in peptidoglycan heteropolymers of the prokaryotes cell walls.		
CC	-!- SUBUNIT: Monomer.		
CC	-!- MICRONECESSARY: Lysozyme C is capable of both hydrolysis and transglycosylation; it shows also a slight esterase activity. It acts rapidly on both peptide-substituted and unsubstituted peptides.		
CC	-!- SIMILARITY: Belongs to family 22 of glycosyl hydrolases.		
DR	DIR; A60525; A60525.		
DR	HSSP; P1376; 2E0L.		
DR	InterPro; IPR00116; Glyco_hydro_22.		
DR	Pfam; PF00052; Lys_Proteins.		
DR	PS00128; LACTALBUMIN_LYSOZYME; PARTIAL.		
KW	Hydrolase; Glycosidase; Bacteriolytic enzyme; Milk.		
FT	NON_TER 20		
SEQ	20 AA;	2314 MW;	EBS824E59425E13 CRC64;

Query Match 81.8%; Score 9; DB 1; Length 20;  
 Best Local Similarity 66.7%; Pred. No. 7.7e+02;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LXR 3  
 Db 8 LAR 10

**RESULT 7**

RECK_AZOVI	STANDARD;	PRT;	20 AA.
ID	RECK_AZOVI		
AC	P37863;		
DT	01-OCT-1994 (Rel. 30, Created)		
DT	01-OCT-1994 (Rel. 30, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Regulatory protein reck (Fragment).		
GN	RECK.		
OS	Azotobacter vinelandii.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;		

FT NON\_TER 1 1 RT "Glutamine synthetase from a cyanobacterium, Phormidium lapideum; purifications, characterization, and comparison with other cyanobacterial enzymes.";

FT NON\_TER 21 21 RT C. J. Biochem. 104: 917-923 (1988).

FT SEQUENCE 21 AA; 2293 MW; D739DDC62CD43375 CRC64; RT CATALYTIC ACTIVITY: ATP + L-glutamate + NH<sub>3</sub> = ADP + phosphate + L-glutamine.

Query Match 81.8%; Score 9; DB 1; Length 21; CC -!- SUBUNIT: Oligomer of 12 subunits arranged in the form of two hexagons.

Best Local Similarity 66.7%; Pred. No. 8.2e+02; 0; Mismatches 1; Indels 0; Gaps 0; CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

Matches 2; Conservative 2; CC -!- SIMILARITY: Belongs to the glutamine synthetase family.

QY 1 LXR 3 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

Db 18 LAR 20 DR PIR: PX0011; PX0011.

RESULT 9 DR InterPro: IPRO0147; Gln\_synth\_beta.

ID\_ANFC\_CHICK STANDARD; PRT; 22 AA. DR InterPro: IPRO08116; Gln\_synth\_C.

AC P21805; DR PROSITE; PS00180; GLNA\_1; PARTIAL.

FT 01-MAY-1991 (Rel. 18, Created) DR PROSITE; PS00181; GLNA\_ATP; PARTIAL.

FT 01-MAY-1991 (Rel. 18, Last sequence update) KW Ligase.

FT 10-OCT-2003 (Rel. 42, Last annotation update) FT NON\_TER 23 DR InterPro: IPRO08117; Gln\_synth\_beta.

C-type natriuretic peptide (CNP). DR PROSITE; PS00182; GLNA\_2; PARTIAL.

GN NPPC. DR PROSITE; PS00183; GLNA\_3; PARTIAL.

OS Gallus gallus (Chicken) DR PROSITE; PS00184; GLNA\_4; PARTIAL.

OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; DR PROSITE; PS00185; GLNA\_5; PARTIAL.

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; DR PROSITE; PS00186; GLNA\_6; PARTIAL.

OC Gallus. DR PROSITE; PS00187; GLNA\_7; PARTIAL.

NCBI\_TaxID=9031; DR PROSITE; PS00188; GLNA\_8; PARTIAL.

RN [1] DR PROSITE; PS00189; GLNA\_9; PARTIAL.

RP SEQUENCE. DR PROSITE; PS00190; GLNA\_10; PARTIAL.

RC TISSUE=Brain; DR PROSITE; PS00191; GLNA\_11; PARTIAL.

RX MEDLINE=91113186; Published=1989595; DR PROSITE; PS00192; GLNA\_12; PARTIAL.

RA Arimura J.-J., Minamino N., Kangawa K., Matsuo H.; DR PROSITE; PS00193; GLNA\_13; PARTIAL.

RT "Isolation and identification of C-type natriuretic peptide in chicken brain."; DR PROSITE; PS00194; GLNA\_14; PARTIAL.

RT chicken brain."; DR PROSITE; PS00195; GLNA\_15; PARTIAL.

RC Biochem. Biophys. Res. Commun. 174:142-148 (1991). DR PROSITE; PS00196; GLNA\_16; PARTIAL.

CC !- FUNCTION: Vasorelaxant activity. Has a cGMP-stimulating activity. DR PROSITE; PS00197; GLNA\_17; PARTIAL.

CC -!- SUBCELLULAR LOCATION: Secreted. DR PROSITE; PS00198; GLNA\_18; PARTIAL.

CC -!- SIMILARITY: Belongs to the natriuretic peptide family. DR PROSITE; PS00199; GLNA\_19; PARTIAL.

PIR: JT0581; JT0581. DR PROSITE; PS00200; GLNA\_20; PARTIAL.

DR InterPro; IPR00063; Natr\_Peptide. DR PROSITE; PS00201; GLNA\_21; PARTIAL.

PRINTS; PR00710; NAT\_PEPIDES. DR PROSITE; PS00202; GLNA\_22; PARTIAL.

SMART; SM00183; NAT\_PEP; 1. DR PROSITE; PS00203; NATRIURETIC\_PEPTIDE; 1.

Vasoactive. DR PROSITE; PS00204; GLNA\_23; PARTIAL.

FT DISULFID 6 22 DR PROSITE; PS00205; GLNA\_24; PARTIAL.

SEQUENCE 22 AA; 2244 MW; FC2A4706DBDAC025 CRC64; DR PROSITE; PS00206; GLNA\_25; PARTIAL.

Query Match 81.8%; Score 9; DB 1; Length 22; CC -!- FUNCTION: Hydrolizes Diposphosphate + H<sub>2</sub>O = 2 phosphate.

Best Local Similarity 66.7%; Pred. No. 8.6e+02; 0; Mismatches 1; Indels 0; Gaps 0; CC -!- COFACTOR: Binds 4 magnesium ions per subunit. Other metal ions can support activity, but at a lower rate. Two magnesium ions are required for the activation of the enzyme and are present before substrate binds, two additional magnesium ions form complexes with substrate and product (By similarity).

Matches 2; Conservative 2; CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

DE (Fragment). CC -!- SIMILARITY: Belongs to the PPase family.

DE Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) DR HAMAP; MF\_00209; -/- 1.

OS Phormidium lapideum. DR HYDROLASE; Metal-binding; Magnesium.

Bacteria; Cyanobacteria; Oscillatoriaceae; Phormidiaceae. DR NON\_TER 25 DR PROSITE; PS00207; GLNA\_26; PARTIAL.

RESULT 10 DR PROSITE; PS00208; GLNA\_27; PARTIAL.

ID\_GINA\_PHOLP STANDARD; PRT; 23 AA. DR PROSITE; PS00209; GLNA\_28; PARTIAL.

AC P20479; DR PROSITE; PS00210; GLNA\_29; PARTIAL.

FT 01-FEB-1991 (Rel. 17, Created) DR PROSITE; PS00211; GLNA\_30; PARTIAL.

FT 01-FEB-1991 (Rel. 17, Last sequence update) DR PROSITE; PS00212; GLNA\_31; PARTIAL.

FT 15-DEC-1998 (Rel. 37, Last annotation update) DR PROSITE; PS00213; GLNA\_32; PARTIAL.

DE Glutamine synthetase (EC 6.3.1.2) (Glutamate--ammonia ligase) DR PROSITE; PS00214; GLNA\_33; PARTIAL.

OS Phormidium lapideum. DR PROSITE; PS00215; GLNA\_34; PARTIAL.

Bacteria; Cyanobacteria; Oscillatoriaceae; Phormidiaceae. DR PROSITE; PS00216; GLNA\_35; PARTIAL.

NCBI\_TaxID=32060; DR PROSITE; PS00217; GLNA\_36; PARTIAL.

RN [1] DR PROSITE; PS00218; GLNA\_37; PARTIAL.

RP SEQUENCE. DR PROSITE; PS00219; GLNA\_38; PARTIAL.

RX MEDLINE=89214011; PubMed=2907514; DR PROSITE; PS00220; GLNA\_39; PARTIAL.

RA Sawa Y., Ochiai H., Yoshida K., Tanizawa K., Tanaka H., Soda K.; DR PROSITE; PS00221; GLNA\_40; PARTIAL.

RESULT 12 DR PROSITE; PS00222; GLNA\_41; PARTIAL.

ID\_NEUTRANTE STANDARD; PRT; 25 AA. DR PROSITE; PS00223; GLNA\_42; PARTIAL.

AC P20056; DR PROSITE; PS00224; GLNA\_43; PARTIAL.

DT 01-FEB-1991 (Rel. 17, Last sequence update)	FT VARIANT 1 3 MISSING (IN N-3 ISOFORM) .
DT 01-FEB-1991 (Rel. 17, Last annotation update)	FT VARIANT 2 5 MISSING (IN C-4 ISOFORM) .
DT 28-FEB-2003 (Rel. 41, Last annotation update)	SQ Sequence AA; 3001 MW; AA9370264265F6 CRC64;
DE Neuronedin U-25 (NmU-25).	
OS Rana temporaria (European common frog).	Query Match 81.8%; Score 9; DB 1; Length 25;
OC Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Euteleostomi;	Best Local Similarity 66.7%; Pred. No. 9.9e+02;
OC Amphiibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana;	Mismatches 0; Indels 0; Gaps 0;
NCBI_TAXID=8407;	
RN [1]	
RP SEQUENCE.	
RC TISSUE_Intestine;	Qy 1 LXR 3
RX MEDLINE=90078179; PubMed=2592357;	Db 22 LTR 24
RA Domini J.J., Yangou Y.G., Spokes R.A., Aitken A., Parmar K.B.,	RESULT 14
RA Chrysanthou B.J., Bloom S.R.,	UBLI_BOVIN STANDARD; PRT; 25 AA.
RT "The distribution, purification, and pharmacological action of an amphibian neuronedin U.";	UBLI_BOVIN P23156;
RT RBL P23156;	AC 01-NOV-1991 (Rel. 20, Created)
CC J. Biol. Chem. 264:20881-20889 (1989).	DT 01-NOV-1991 (Rel. 20, Last sequence update)
CC -!- FUNCTION: Stimulates uterine smooth muscle contraction and causes selective vasoconstriction.	DT 15-MAR-2004 (Rel. 43, Last annotation update)
CC -!- SIMILARITY LOCATION: Secreted.	DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-L1) (Ubiquitin thiolesterase L1) (Neuron cytoplasmic protein 9.5) (PGP 9.5) (Fragment).
CC -!- SIMILARITY LOCATION: Belongs to the NmU family.	DE DE (PGP 9.5) (PGP9.5) (Fragment).
DR PIR; A34179; A34179.	GN UCHL1.
DR InterPro; IPR008199; NmU; 1.	OS Bos taurus (Bovine).
DR SMART; SM00084; NmU; 1.	OC Meizaoza; Chordata; Vertebrata; Buteleostomi;
DR PROSITE; PS00967; NmU; 1.	OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
KW Amidation; Hormone.	OC Bovidae; Bovinae; Bos.
FT MOD RES 25 AMIDATION.	NCBI_TaxID=9913;
SQ SEQUENCE 25 AA; 2832 MW;	OX
RP SEQUENCE 25 AA; 2832 MW;	RN [1]
Query Match 81.8%; Score 9; DB 1; Length 25;	RP SEQUENCE.
Best Local Similarity 66.7%; Pred. No. 9.9e+02;	RC TISSUE_Brain;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	RX MEDLINE=92008646; PubMed=1833240;
Qy 1 LXR 3	RA Gianfranco I., Bianchi R., Ceccarelli P., Pula G., Sorci G.,
Db 14 LSR 16	RA Antonioli S., Bocchini V., Donato R.,
RESULT 13	RT "Neuron specific" protein gene product 9.5 (PGP 9.5) is also expressed in glioma cell lines and its expression depends on cellular growth state.;
SPIG_PSEUS STANDARD; PRT; 25 AA.	RL FEBS Lett. 290:1131-1134 (1991).
ID SPIG_PSEUS	CC CC Processing of ubiquitin-protein hydrolase is involved both in the processing of ubiquitin precursors and of ubiquinated proteins. This enzyme is a thiol protease that recognizes and hydrolyzes a peptide bond at the C-terminal Glycine of ubiquitin.
AC P23571	CC CC A peptide bond + a thiol.
AC P23571	CC CC -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O = ubiquitin + a thiol.
AC P23571	CC CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
AC P23571	CC CC -!- TISSUE SPECIFICITY: Neurons and cells of the diffuse neuroendocrine system and their tumors.
AC P23571	CC CC -!- SIMILARITY: Belongs to Peptidase Family C12.
AC P23571	CC DR PIR; S17561; S17561.
AC P23571	CC DR MEROPS; C12.001; -
AC P23571	CC DR InterPro; IPR001578; Peptidase_C12.
AC P23571	CC DR Pfam; PF0118; Peptidase_C12; _
AC P23571	CC DR PROSITE; PS00140; UCH_1; PARTIAL.
AC P23571	CC KW Ub1 conjugation pathway; Hydrolase; Thiol protease; Multigene family.
AC P23571	CC PT NON_TER 25 25
AC P23571	CC SQ SEQUENCE 25 AA; 2812 MW; 26BB5ADD0A754D55 CRC64;
RA Lambert M., Zacheiry D., Lanot R., Bordereau C., Robert A., Hoffmann J.A., Bulet P.,	Query Match 81.8%; Score 9; DB 1; Length 25;
RA "Insect Immunity. Constitutive expression of a cysteine-rich antifungal and a linear antibacterial peptide in a termite insect."	Best Local Similarity 66.7%; Pred. No. 9.9e+02;
RT DE Springerin.	Mismatches 0; Indels 0; Gaps 0;
OS Pseudocanthotermes spiniger.	
OC Eukarya; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neuroptera; Orthopteroidea; Dictyoptera; Isoptera; Termitidae; Macrotermitinae; Pseudocanthotermes.	
OC NCBI_TAXID=115113;	
RN [1]	
RP SEQUENCE MASS SPECTROMETRY, AND FUNCTION.	
RC TISSUE_Blood, and Salivary Gland;	
RX PubMed=11053427;	
RA Lambert M., Zacheiry D., Lanot R., Bordereau C., Robert A., Hoffmann J.A., Bulet P.,	
RA "Insect Immunity. Constitutive expression of a cysteine-rich antifungal and a linear antibacterial peptide in a termite insect."	
RT DE J. Biol. Chem. 276:4088-4092 (2001)	
CC -!- FUNCTION: Active against Gram-positive bacteria <i>B. megaterium</i> and <i>M. luteus</i> . Gram-negative bacteria <i>E. coli</i> SB363 and D22,	
CC K. pneumoniae, <i>S. typhimurium</i> and <i>P. aeruginosa</i> , yeast <i>C. albicans</i> and filamentous fungi <i>F. culmorum</i> , <i>N. crassa</i> , <i>N. hematococca</i> and <i>T. viridae</i> . Inactive against Gram-positive bacteria <i>B. subtilis</i> , <i>S. xylosides</i> , <i>B. thuringiensis</i> and <i>S. auraus</i> . Gram-negative bacteria <i>E. cloacae</i> and <i>E. carotovora</i> and filamentous fungus <i>B. bassiana</i> .	
CC -!- SUBCELLULAR LOCATION: Secreted.	
CC -!- INDUCTION: By bacterial infection.	
CC -!- MASS SPECTROMETRY: MW=3001.8; METHOD=MALDI	
CC -!- MISCELLANEOUS: There are three isoforms of spingerin.	
KW Antibiotic; Fungicide.	

DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Nitrogen assimilation regulatory protein (Fragment).  
GN NTRC  
OS Rhizobium leguminosarum (biovar phascoli).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.  
NCBI\_TaxID=385;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CE-3;  
RX MEDLINE=94018651; PubMed=8412703;  
RA Patriarca E.J., Riccio A., Tate R., Colonna-Romano S., Iaccarino M.,  
RA Defez R.;  
RT "The ntrBC genes of Rhizobium leguminosarum are part of a complex  
operon subject to negative regulation.";  
RL Mol. Microbiol. 9:569-577(1993).  
-1 FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM NTRB/NTRC  
CC INVOLVED IN THE ACTIVATION OF NITROGEN ASSIMILATORY GENES SUCH AS  
CC GlnA. NTRC IS PHOSPHORYLATED BY NTRB AND INTERACTS WITH SIGMA-54.  
CC -1 SIMILARITY: Contains 1 response regulatory domain.  
CC  
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CC  
DR EMBL; X71436; -; NOT\_ANNOTATED\_CDS.  
DR PIR; S3203; S3623; Response reg.  
DR PROSITE; PSS0110; RESPONSE\_REGULATOR; 1.  
KW Nitrogen fixation; Transcription regulation; Repressor; Activator;  
KW DNA-binding; ATP-binding; Phosphorylation; Sensory transduction.  
FT DOMAIN 1 >26 RESPONSE\_REGULATOR.  
FT NON\_TER 26 26  
SQ SEQUENCE 26 AA; 2687 MW; E1BCC63C8636304 CRC64;  
Query Match 81.8%; Score 9; DB 1; Length 26;  
Best Local Similarity 66.7%; Pred. No. 1e+03;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 LXR 3  
Db 22 LSR 24

Result No.	Score	Query	Match	Length	DB	ID	Description
1	9	Q94vfo varanus kin	Q16468 homo sapien	8	4	Q16468	Q9t4y2 asterina pe
2	9	Gencore version 5.1.6	Q9t4y2	8	8	Q9t4y2	Q9t945 polyomaviru
3	9	Copyright (c) 1993 - 2004 Compugen Ltd.	Q9t945	8	12	Q9t945	Q9t688 gecko gecko
4	9	OM protein - protein search, using sw model	Q9t688	9	8	Q9t688	Q94vh4 varanus gila
5	9	Run on: September 24, 2004, 07:28:32 ; Search time 4.16842 Seconds	Q9t688	9	8	Q94vh4	Q94v8 varanus nil
6	9	(without alignments)	Q9t688	9	8	Q94v8	Q94vc8 varanus ere
7	9	302.770 Million Cell updates/sec	Q9t688	9	8	Q94vc6	Q94vc6 varanus pil
8	9	Searched: US-09-498-556C-357	Q9t688	9	8	Q94vc6	Q94vc6 varanus mer
9	9	Perfect score: 11	Q9t688	9	12	Q9t688	Q9t688 simian viru
10	9	Sequence: 1 LXRX 4	Q9t688	9	12	Q9t688	O9pyk1 simian viru
11	9	Scoring table: BLOSUM62.	Q9t688	9	10	Q9t688	O958g rana boylii
12	9	Gapop 10.0 , Gapext 0.5	Q9t688	9	10	Q9t688	O9tg86 diploglossu
13	9	Total number of hits satisfying chosen parameters:	1017041	1	1	Q9t688	Q94v97 varanus spe
14	9	Minimum DB seq length: 0	0	1	1	Q9t688	Q94vd5 varanus oli
15	9	Maximum DB seq length: 200000000	0	1	1	Q9t688	Q94vg8 varanus gou
16	9	Post-processing: Minimum Match 0%	0	1	1		
		Maximum Match 100%	0	1	1		
		Listing first 45 summaries	0	1	1		
		SPREMBL_25:*	0	1	1		
		1: sp_archaea:*	0	1	1		
		2: sp_bacteria:*	0	1	1		
		3: sp_fungi:*	0	1	1		
		4: sp_human:*	0	1	1		
		5: sp_invertebrate:*	0	1	1		
		6: sp_mammal:*	0	1	1		
		7: sp_mhc:*	0	1	1		
		8: sp_organelle:*	0	1	1		
		9: sp_phage:*	0	1	1		
		10: sp_plant:*	0	1	1		
		11: sp_rat:*	0	1	1		
		12: sp_virus:*	0	1	1		
		13: sp_vertebrate:*	0	1	1		
		14: sp_unclassified:*	0	1	1		
		15: sp_virus:*	0	1	1		
		16: sp_bacteriaph:*	0	1	1		
		17: sp_archeap:*	0	1	1		
		SUMMARIES	0	1	1		
		RESULT 1	0	1	1		
		Q16468	0	1	1		
		ID Q16468	0	1	1		
		PRELIMINARY;	0	1	1		
		PRT;	0	1	1		
		8 AA.	0	1	1		
		ALIGMENTS	0	1	1		
		RP SEQUENCE FROM N.A.	0	1	1		
		RX MEDLINE=643520; PubMed=8838806;	0	1	1		
		RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J., Anand R.; Created)	0	1	1		
		RA Last sequence update)	0	1	1		
		DT 01-MAY-1996 (TREMBLrel.	0	1	1		
		DT 01-MAY-1999 (TREMBLrel.	0	1	1		
		DT 01-JUN-2003 (TREMBLrel.	0	1	1		
		DE DNA for cosmid cc13.13-13.24, Last (Fragment).	0	1	1		
		OS Homo sapiens (Human).	0	1	1		
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	0	1	1		
		OX NCBI_TaxID=9606;	0	1	1		
		RN [1]	0	1	1		
		SEQUENCE FROM N.A.	0	1	1		
		RX MEDLINE=643520; PubMed=8838806;	0	1	1		
		RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J., Anand R.; Created)	0	1	1		
		RA Last sequence update)	0	1	1		
		DT 01-MAY-1996 (TREMBLrel.	0	1	1		
		DT 01-MAY-1999 (TREMBLrel.	0	1	1		
		DT 01-JUN-2003 (TREMBLrel.	0	1	1		
		DE DNA for cosmid cc13.13-13.24, Last (Fragment).	0	1	1		
		OS Homo sapiens (Human).	0	1	1		
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	0	1	1		
		OX NCBI_TaxID=9606;	0	1	1		
		RN [1]	0	1	1		
		SEQUENCE FROM N.A.	0	1	1		
		RX MEDLINE=643520; PubMed=8838806;	0	1	1		
		RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J., Anand R.; Created)	0	1	1		
		RA Last sequence update)	0	1	1		
		DT 01-MAY-1996 (TREMBLrel.	0	1	1		
		DT 01-MAY-1999 (TREMBLrel.	0	1	1		
		DT 01-JUN-2003 (TREMBLrel.	0	1	1		
		DE DNA for cosmid cc13.13-13.24, Last (Fragment).	0	1	1		
		OS Homo sapiens (Human).	0	1	1		
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	0	1	1		
		OX NCBI_TaxID=9606;	0	1	1		
		RN [1]	0	1	1		
		SEQUENCE FROM N.A.	0	1	1		
		RX MEDLINE=643520; PubMed=8838806;	0	1	1		
		RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J., Anand R.; Created)	0	1	1		
		RA Last sequence update)	0	1	1		
		DT 01-MAY-1996 (TREMBLrel.	0	1	1		
		DT 01-MAY-1999 (TREMBLrel.	0	1	1		
		DT 01-JUN-2003 (TREMBLrel.	0	1	1		
		DE DNA for cosmid cc13.13-13.24, Last (Fragment).	0	1	1		
		OS Homo sapiens (Human).	0	1	1		
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	0	1	1		
		OX NCBI_TaxID=9606;	0	1	1		
		RN [1]	0	1	1		
		SEQUENCE FROM N.A.	0	1	1		
		RX MEDLINE=643520; PubMed=8838806;	0	1	1		
		RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J., Anand R.; Created)	0	1	1		
		RA Last sequence update)	0	1	1		
		DT 01-MAY-1996 (TREMBLrel.	0	1	1		
		DT 01-MAY-1999 (TREMBLrel.	0	1	1		
		DT 01-JUN-2003 (TREMBLrel.	0	1	1		
		DE DNA for cosmid cc13.13-13.24, Last (Fragment).	0	1	1		
		OS Homo sapiens (Human).	0	1	1		
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		OX NCBI_TaxID=9606;	0	1	1		
		RN [1]	0	1	1		
		SEQUENCE FROM N.A.	0	1	1		
		RX MEDLINE=643520; PubMed=8838806;	0	1	1		
		RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J., Anand R.; Created)	0	1	1		
		RA Last sequence update)	0	1	1		
		DT 01-MAY-1996 (TREMBLrel.	0	1	1		
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		OS Homo sapiens (Human).	0	1	1		
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		OX NCBI_TaxID=9606;	0	1	1		
		RN [1]	0	1	1		
		SEQUENCE FROM N.A.	0	1	1		
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		RA Last sequence update)	0	1	1		
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		DT 01-MAY-1999 (TREMBLrel.	0	1	1		
		DT 01-JUN-2003 (TREMBLrel.	0	1	1		
		DE DNA for cosmid cc13.13-13.24, Last (Fragment).	0	1	1		
		OS Homo sapiens (Human).	0	1	1		
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	0	1	1		
		OX NCBI_TaxID=9606;	0	1	1		
		RN [1]	0	1	1		
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		RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J., Anand R.; Created)	0	1	1		
		RA Last sequence update)	0	1	1		
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		DT 01-MAY-1999 (TREMBLrel.	0	1	1		
		DT 01-JUN-2003 (TREMBLrel.	0	1	1		
		DE DNA for cosmid cc13.13-13.24, Last (Fragment).	0	1	1		
		OS Homo sapiens (Human).	0	1	1		
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	0	1	1		
		OX NCBI_TaxID=9606;	0	1	1		
		RN [1]	0	1	1		
		SEQUENCE FROM N.A.	0	1	1		
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		RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J., Anand R.; Created)	0	1	1		
		RA Last sequence update)	0	1	1		
		DT 01-MAY-1996 (TREMBLrel.	0	1	1		
		DT 01-MAY-1999 (TREMBLrel.	0	1	1		
		DT 01-JUN-2003 (TREMBLrel.	0	1	1		
		DE DNA for cosmid cc13.13-13.24, Last (Fragment).	0	1	1		
		OS Homo sapiens (Human).	0	1	1		
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		OX NCBI_TaxID=9606;	0	1	1		
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		SEQUENCE FROM N.A.	0	1	1		
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		RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J., Anand R.; Created)	0	1	1		
		RA Last sequence update)	0	1	1		
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		DE DNA for cosmid cc13.13-13.24, Last (Fragment).	0	1	1		
		OS Homo sapiens (Human).	0	1	1		
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo.	0	1	1		
		OX NCBI_TaxID=9606;	0	1	1		
		RN [1]	0	1	1		
		SEQUENCE FROM N.A.	0	1	1		
		RX MEDLINE=643520; PubMed=8838806;	0	1	1		
		RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J., Anand R.; Created)	0	1	1		
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		OX NCBI_TaxID=9606;	0	1	1		
		RN [1]	0	1	1		
		SEQUENCE FROM N.A.	0	1	1		
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		RA James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J., Anand R.; Created)	0	1	1		
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		DT 01-MAY-1999 (TREMBLrel.	0	1	1		
		DT 01-JUN-2003 (TREMBLrel.	0	1	1		

DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	OC	Lepidosauria; Squamata; Scincoglossa; Gekkota; Gekkonidae; Gekko.
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)	OX	NCBI_TaxID=36310;
DE	COI gene product (Fragment);	RN	SEQUENCE FROM N.A.
OS	Asterina pectinifera (Starfish).	RP	SEQUENCE FROM N.A.
OG	Mitochondrion.	RX	MEDLINE:99341618; PubMed:10413626;
OC	Eukaryota; Metazoa; Echinodermata; Blepherozoa; Asterozoa;	AC	Macy J.R., Wang Y., Ananjeva N.B., Larson A., Papenfuss T.J.;
OC	Astrocoidea; Valvatacea; Valvatida; Asterinidae; Asterina.	RT	"Conserved patterns of fragmentation among gekkonid lizards of the genus <i>Tetrascincus</i> produced by the Indian collision: A molecular phylogenetic perspective and an area Cladogram for central asia.";
OX	[1]	RT	Genus <i>Tetrascincus</i> produced by the Indian collision: A molecular phylogenetic perspective and an area Cladogram for central asia.";
RN	NCBI_TaxID=7594;	RT	Phylogenetic analysis of gekkonid lizards of the Indian collision: A molecular phylogenetic perspective and an area Cladogram for central asia.";
RP	SEQUENCE FROM N.A.	RL	Mol. Phylogen. Evol. 12:320-332(1999).
RX	MLINE:89354669; PubMed:216388;	DR	EMBL; AF114249; AAD5100.1;
RA	Jacobs H.T., Asakawa S., Araki T., Miura K., Smith M.J., Watanabe K.,	GO	GO:0005739; C:mitochondrion; IEA.
RT	"Conserved tRNA gene cluster in starfish mitochondrial DNA.";	RW	Mitochondrion.
RL	Curr. Genet. 15:193-206 (1989).	FT	NON TER
DR	EMBL; X16886; CA034767.1;	SQ	SEQUENCE 9 AA; 1188 MW; 428CB9C9D36411A7 CRC64;
DR	GO:0005739; C:mitochondrion; IEA.	Query Match	Score 9; DB 8; Length 9;
KW	Mitochondrion.	Best Local Similarity	61.8%; Score 9; DB 8; Length 9;
FT	NON TER	Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Matches 2; Conservative 0; Mismatches 0; Pred. No. 1e+06; Pred. No. 1e+06;
SQ	SEQUENCE 8 AA; 1114 MW; POC9D36415B736D6 CRC64;	QY	1 LXR 3
QY	1 LXR 3	Db	2 LTR 4
Db	3 LSR 5	RESULT 5	Q94VH4
Db	3 LSR 5	ID	Q94VH4
Db	3 LSR 5	AC	Q94VH4;
Db	3 LSR 5	DT	Q1-DEC-2001 (TREMBLrel. 19, Created)
Db	3 LSR 5	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
Db	3 LSR 5	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
Db	3 LSR 5	DE	Cytochrome c oxidase subunit I (Fragment).
Db	3 LSR 5	GN	Varanus glauerti.
Db	3 LSR 5	GO	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	3 LSR 5	OC	Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
Db	3 LSR 5	NCBI_TaxID=169841;	[1]
Db	3 LSR 5	RN	SEQUENCE FROM N.A.
Db	3 LSR 5	RP	At J.C.;
Db	3 LSR 5	RA	"Mitochondrial DNA evidence and evolution in varanoids (Squamata)." ;
Db	3 LSR 5	RL	Cladistics 17:0-0(2001).
Db	3 LSR 5	DR	EMBL; AF407500; AAL10054.1;
Db	3 LSR 5	GO	GO:0005739; C:mitochondrion; IEA.
Db	3 LSR 5	RW	Mitochondrion.
Db	3 LSR 5	FT	NON TER
Db	3 LSR 5	SQ	SEQUENCE 9 AA; 1124 MW; 9E80C733640DD731 CRC64;
Db	3 LSR 5	Query Match	Score 9; DB 8; Length 9;
Db	3 LSR 5	Best Local Similarity	61.8%; Score 9; DB 8; Length 9;
Db	3 LSR 5	Matches 2; Conservative 0; Mismatches 0; Pred. No. 1e+06; Pred. No. 1e+06;	Matches 2; Conservative 0; Mismatches 0; Pred. No. 1e+06; Pred. No. 1e+06;
Db	3 LSR 5	QY	1 LXR 3
Db	3 LSR 5	Db	3 LAR 5
Db	3 LSR 5	RESULT 6	Q94VDB
Db	3 LSR 5	ID	Q94VDB
Db	3 LSR 5	AC	Q94VDB;
Db	3 LSR 5	DT	Q1-DEC-2001 (TREMBLrel. 19, Created)
Db	3 LSR 5	DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
Db	3 LSR 5	DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
Db	3 LSR 5	DE	Cytochrome c oxidase subunit I (Fragment).
Db	3 LSR 5	GN	COI.
Db	3 LSR 5	OS	Varanus niloticus (Nile monitor).
Db	3 LSR 5	OG	Mitochondrion.
Db	3 LSR 5	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db	3 LSR 5	OC	Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
Db	3 LSR 5	OC	NCBI_TaxID=62046;
Db	3 LSR 5	OC	NCBI_TaxID=36310;

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[1] DN DR EMBL; AF07518; AAU10108.1; -
  RP GO; GO:0005339; C:mitochondrion; IEA.
  AST J.C.; KRW Mitochondrion.
  RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
  Cladistics 17:0 (2001).
  EMBL; AF07514; AAL10096..1;
  GO; GO:0005739; C:mitochondrion; IEA.
  DR Mitochondrion.
  KW NON_TER 9
  SQ SEQUENCE 9 AA; 1154 MW; 874CA5A36411A715 CRC64;
  Query Match 81.8%; Score 9; DB 8; Length 9;
  Best Local Similarity 66.7%; Pred. No. 1e+06;
  Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 1 LXR 3
  DB 3 LTR 5
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  ID Q94VE1
  AC Q94VE1;
  DT 01-DEC-2001 (TrEMBLrel. 19, Created)
  DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
  DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
  DE Cytochrome c oxidase subunit I (Fragment).
  GN COI.
  OS Varanus meridionalis (Mertens' water monitor).
  OG Mitochondrion.
  OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus;
  OX NCBI_TaxID:62044;
  RN [1]
  RP SEQUENCE FROM N.A.
  RA Ast J.C.;"Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
  RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
  RL Cladistics 17:0-0(2001).
  DR EMBL; AF40795; AAL10040.1;
  GO; GO:0005739; C:mitochondrion; IEA.
  DR Mitochondrion.
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  SQ SEQUENCE 9 AA; 1124 MW; 9E80C7336410DD731 CRC64;
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  Best Local Similarity 66.7%; Pred. No. 1e+06;
  Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 1 LXR 3
  DB 3 LTR 5
  RESULT 10
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  AC Q9IBMB8;
  DT 01-OCT-2000 (TrEMBLrel. 15, Created)
  DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
  DE control region (Fragment).
  DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
  DE Papovavirus BK (Gardner derived clone BK9) early transcription
  OS Simian virus 12.
  OX NCBI_TaxID=6771;
  RN [1]
  RP SEQUENCE FROM N.A.
  RC STRAIN_Gardner;
  RX MEDLINE=87061221; PubMed=1023684;
  RA Chuke W.P., Walker D.L., Peitzman L.B., Frisque R.J.;"Construction and characterization of hybrid Polymavirus genomes.";
  RT "Construction and characterization of hybrid Polymavirus genomes.";
  RL Virch. 60:960-971(1986).
  DR EMBL; M14452; AAA96256.1;
  FT NON_TER 9
  SQ SEQUENCE 9 AA; 1130 MW; C7FDD15B736C40732 CRC64;
  Query Match 81.8%; Score 9; DB 12; Length 9;

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Qy	1 LXR 3 6 LSR 8	Best Local Similarity 66.7%; Pred. No. 1e+06; Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Db	3 LTR 5
RESULT 11			RESULT 13	
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DT 01-MAY-2000 (TREMBLrel. 13, Created)			AC Q9TGS6;	
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)			ID 01-MAY-2000 (TREMBLrel. 13, Created)	
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)			DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)			DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DE Papovavirus BK (Gardner) early transcription control region (Fragment).			DE Cytochrome c oxidase subunit I (Fragment).	
DE Simian virus 12.			GN COI.	
OS Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.			OS Diploglossus bilobatus.	
OX NCBI_TaxID:46771;			OG Mitochondrion.	
RN [1]			OC Lepidosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Anguillidae; Diploglossus.	
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RC STRAIN=Gardner;			RN [1]	
RX MEDLINE=87061221; PubMed=3023684;			RP SEQUENCE FROM N.A.	
RA Chuке W.F., Walker D.L., Peitman L.B., Frisque R.J.;"			RX MEDLINE=99433612; PubMed=10413621;	
RT "Construction and characterization of hybrid polyomavirus genomes."			RA Macey J.R., Schulte J.A. II, Larson A., Tuneyev B.S., Orlov N., Papenfuss T. J.;	
DE Papovavirus BK (Gardner) early transcription control region (Fragment).			RT "Molecular phylogenetics, tRNA evolution, and historical biogeography in anguid lizards and related taxonomic families.";	
DR EMBL: M14451; AAA9635.1; -.			RL Mol. Phylogenet. Evol. 12:250-272(1999).	
FT NON-TER 9 AA; 1130 MW; C7FD15B736C40732 CRC64;			DR EMBL; AF085608; AD51514.1; -.	
SQ SEQUENCE 9 AA; 1130 MW;			DR GO:0005739; C:mitochondrion; IEA.	
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Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			FT NON-TER 10 AA; 1255 MW; 5D8E80C7336411A7 CRC64;	
Qy 1 LXR 3 6 LSR 8			SQ SEQUENCE 10 AA; 1255 MW;	
Db			Query Match Score 9; DB 8; Length 10; Best Local Similarity 66.7%; Pred. No. 4.7e+03; Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
RESULT 12			Qy 1 LXR 3 3 LTR 5	
Q958K9	PRELIMINARY;	PRT; 10 AA.	Db	
AC Q958K9;			RESULT 14	
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DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			ID Q94V97;	PRT; 10 AA.
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)			AC Q94V97;	
DB Cytochrome c oxidase subunit I (Fragment).			ID 01-DEC-2001 (TREMBLrel. 19, Created)	
GN COI.			DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
OS Rana boillii.			DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
CG Mitochondrion.			DE Cytochrome c oxidase subunit I (Fragment).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.			GN COI.	
OX NCBI_TaxID:160499;			OS varanus spenceri.	
RN [1]			OG Mitochondrion.	
RP SEQUENCE FROM N.A.			OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.	
RA Macey J. R., Strasburg J.L., Brisson J.A., Vredenburg V.T., Jennings M., Larson A.;"			NCBI_TaxID:169854;	
RT "Molecular phylogenetics of Western North American Frogs of the Rana boillii Species Group.";			RN [1]	
RT Mol. Phylogen. Evol. 19:131-143(2001).			RP SEQUENCE FROM N.A.	
DR EMBL; AF314019; AAK56877.1; -.			RA Ast J.C.; RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata)." Cladistics 17:0-0(2001).	
GO; GO:0005739; C:mitochondrion; IEA.			PL DR EMBL; AF40530; AAL0142.1; -.	
KW Mitochondrion.			DR GO:0005739; C:mitochondrion; IEA.	
FT NON-TER 10 AA; 1320 MW; 42D380C9D36411A7 CRC64;			KW Mitochondrion.	
SQ SEQUENCE 10 AA;			FT NON-TER 10 AA; 1255 MW; 5D8E80C7336411A7 CRC64;	
Query Match Score 9; DB 8; Length 10; Best Local Similarity 66.7%; Pred. No. 4.7e+03; Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			Query Match Score 9; DB 8; Length 10; Best Local Similarity 66.7%; Pred. No. 4.7e+03; Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy 1 LXR 3			Qy 1 LXR 3	

Db 3 LTR 5

RESULT 15  
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AC ;  
DT 01-DEC-2001 (TREMBUREL 19, Created)  
DT 01-DEC-2001 (TREMBUREL 19, Last sequence update)  
DT 01-JUN-2003 (TREMBUREL 24, Last annotation update)  
DE Cytochrome c oxidase subunit I (Fragment).  
COI.  
OS Varanus olivaceus (Gray's monitor).  
OG Mitochondrion.  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.  
GN NCBI\_TaxID=6204 ;  
RN [1] —  
RP SEQUENCE FROM N.A.  
RA Ast J.C.;  
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata)." ;  
RL Cladistics 17:0-0 (2001).  
DR EMBL; AP407515; AAL10099\_1;  
DR GO:0005739; C:mitochondrion; IEA.  
KW Mitochondrion.  
PT NON\_TER; 10 10  
SQ SEQUENCE 10 AA; 1234 MW; 584C4CA5A36411A7 CRC64;  
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Best Local Similarity 66.7%; Pred. No. 4.7e+03;  
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|  
Db 3 LTR 5

Search completed: September 24, 2004, 07:30:28  
Job time : 7.16842 secs

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